

10561236

# Document made available under the Patent Cooperation Treaty (PCT)

International application number: PCT/US04/020491

International filing date: 25 June 2004 (25.06.2004)

Document type: Certified copy of priority document

Document details: Country/Office: US  
Number: 60/497,649  
Filing date: 25 August 2003 (25.08.2003)

Date of receipt at the International Bureau: 10 September 2004 (10.09.2004)

Remark: Priority document submitted or transmitted to the International Bureau in compliance with Rule 17.1(a) or (b)



World Intellectual Property Organization (WIPO) - Geneva, Switzerland  
Organisation Mondiale de la Propriété Intellectuelle (OMPI) - Genève, Suisse

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APPLICATION NUMBER: 60/497,649

FILING DATE: *August 25, 2003*

RELATED PCT APPLICATION NUMBER: PCT/US04/20491

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"Express Mail" Mailing Label No. EV 351355139 US

Date of Deposit: August 25, 2003

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Lisa M. Nash

Date: August 25, 2003

14230 U.S. PTO  
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1970 60/497649

### PROVISIONAL APPLICATION COVER SHEET

This is a request for a PROVISIONAL APPLICATION under 37 CFR 1.53(c).

Docket No. 20662.002	Type a plus sign (+) inside this box →	+
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#### TITLE OF INVENTION (280 characters max)

Immunogenic Compositions for *Chlamydia trachomatis*

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#### ENCLOSED APPLICATION PARTS (check all that apply)

<input checked="" type="checkbox"/> Specification	Number of Pages: (39 pages)
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<input type="checkbox"/> Drawing(s)	Number of Pages:
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<input type="checkbox"/> Small Entity Statement
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<input type="checkbox"/> Other (specify)
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#### METHOD OF PAYMENT (check one)

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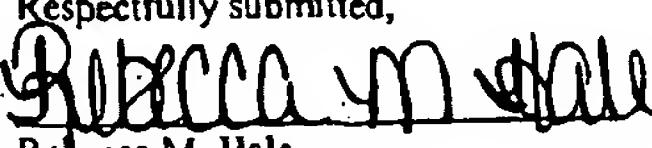
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The invention was made by an agency of the United States Government or under a contract with an agency of the United States government.

No

Yes, the name of the U.S. Government agency and the Government contract number are:

August 25, 2003  
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## IMMUNOGENIC COMPOSITIONS FOR *CHLAMYDIA TRACHOMATIS*

All documents cited herein are incorporated by reference in their entirety.

### TECHNICAL FIELD

This invention is in the fields of immunology and vaccinology. In particular, it relates to antigens  
5 derived from *Chlamydia trachomatis* and their use in immunisation.

### BACKGROUND ART

The *Chlamydiae* are obligate intracellular parasites of eukaryotic cells which are responsible for endemic sexually transmitted infections and various other disease syndromes. They occupy an exclusive eubacterial phylogenetic branch, having no close relationship to any other known organisms.

10 Historically, the *Clamydiae* have been classified in their own order (*Chlamydiales*) made up of a single family (*Chlamydaceae*) which in turn contains a single genus (*Chlamydia*, also referred to as *Chlamydophila*). More recently, this order has been divided into at least four families including *Chlamydaceae*, *Parachlamydaceae*, *Waddiaceae* and *Simkaniaceae*. In this more recent classification, the *Chlamydaceae* family includes genera of *Chlamydophila* and *Chlamydia*,  
15 *Chlamydia trachomatis* being a species within the *Chlamydia* genus. See Ref. 1.

A particular characteristic of the *Chlamydiae* is their unique life cycle, in which the bacterium alternates between two morphologically distinct forms: an extracellular infective form (elementary bodies, EB) and an intracellular non-infective form (reticulate bodies, RB). The life cycle is completed with the re-organization of RB into EB, which leave the disrupted host cell ready to infect  
20 further cells.

The genome sequences of at least five chlamydia or chlamydophila species are currently known – *C.trachomatis*, *C.pneumoniae*, *C.muridarum*, *C.pecorum* and *C.psittaci* (See Refs. 2, 8).

The human serovariants ("serovars") of *C.trachomatis* are divided into two biovariants ("biovars"). Serovars A-K elicit epithelial infections primarily in the ocular tissue (A-C) or urogenital tract  
25 (D-K). Serovars L1, L2 and L3 are the agents of invasive lymphogranuloma venereum (LGV).

Although chlamydial infection itself causes disease, it is thought that the severity of symptoms in some patients is actually due to an aberrant host immune response. Failure to clear the infection results in persistent immune stimulation and, rather than helping the host, this results in chronic infection with severe consequences, including sterility and blindness. See, e.g., Ref. 9. In addition,  
30 the protection conferred by natural chlamydial infection is usually incomplete, transient, and strain-specific.

Due to the serious nature of the disease, there is a desire to provide suitable vaccines. These may be useful (a) for immunisation against chlamydial infection or against chlamydia-induced disease (prophylactic vaccination) or (b) for the eradication of an established chronic chlamydial infection (therapeutic vaccination). Being an intracellular parasite, however, the bacterium can generally evade 5 antibody-mediated immune responses.

Various antigenic proteins have been described for *C.trachomatis*, and the cell surface in particular has been the target of detailed research. See, e.g., Ref. 10. These include, for instance, Pgp3 (Refs. 11, 12, and 13), MOMP (Ref. 14), Hsp60 (GroEL) (Ref. 15) and Hsp70 (DnaK-like) (Ref. 16). Not all of these have proved to be effective vaccines, however, and further candidates have been 10 identified. See Ref. 17.

Vaccines against pathogens such as hepatitis B virus, diphtheria and tetanus typically contain a single protein antigen (e.g. the HBV surface antigen, or a tetanus toxoid). In contrast, acellular whooping cough vaccines typically have at least three *B.pertussis* proteins, and the Prevnar<sup>TM</sup> pneumococcal vaccine contains seven separate conjugated saccharide antigens. Other vaccines such as cellular pertussis vaccines, the measles vaccine, the inactivated polio vaccine (IPV) and meningococcal OMV vaccines are by their very nature complex mixtures of a large number of antigens. Whether protection can be elicited by a single antigen, a small number of defined antigens, or a complex mixture of undefined antigens, therefore depends on the pathogen in question. 15

It is an object of the invention to provide further and improved compositions for providing immunity 20 against chlamydial disease and/or infection. The compositions are based on a combination of two or more (e.g. three or more) *C.trachomatis* antigens.

#### DISCLOSURE OF THE INVENTION

Within the ~900 proteins described for the *C.trachomatis* genome of reference 5, Applicants have discovered a group of five *Chlamydia trachomatis* antigens that are particularly suitable for 25 immunisation purposes, particularly when used in combinations. The invention therefore provides a composition comprising a combination of *Chlamydia trachomatis* antigens, said combination consisting of two, three, four or all five *Chlamydia trachomatis* antigens of a first antigen group; said first antigen group consisting of: (1) PepA; (2) LcrE; (3) ArtJ; (4) DnaK; and (5) CT398. These antigens are referred to herein as the 'first antigen group'.

30 Preferably, the composition of the invention comprises a combination of *Chlamydia trachomatis* antigens, said combination selected from the group consisting of: (1) PepA & LcrE; (2) PepA & ArtJ; (3) PepA & DnaK; (4) PepA & CT398; (5) LcrE & ArtJ; (6) LcrE & DnaK; (7) LcrE & CT398; (8) ArtJ & DnaK; (9) ArtJ & CT398; (10) DnaK & CT398; (11) PepA, LcrE & ArtJ; (12) PepA, LcrE & DnaK; (13) PepA, LcrE & CT398; (14) PepA, ArtJ & DnaK; (15) PepA, ArtJ and CT398;

(16) PepA, DnaK & CT398; (17) LcrE, ArtJ & DnaK; (18) LcrE, ArtJ & CT398; (19) LcrE, DnaK & CT398; (20) ArtJ, DnaK & CT398; (21) PepA, LcrE, ArtJ & DnaK; (22) PepA, LcrE, DnaK & CT398; (23) PepA, ArtJ, DnaK & CT398; (24) PepA, LcrE, ArtJ & CT398; (25) LcrE, ArtJ, DnaK & CT398; and (26) PepA, LcrE, ArtJ, DnaK & CT398. Preferably, the composition of *Chlamydia trachomatis* antigens consists of PepA, LcrE, ArtJ, DnaK & CT398.

The invention also provides for a slightly larger group of 13 *Chlamydia trachomatis* antigens that are particularly suitable for immunisation purposes, particularly when used in combinations. (This second antigen group includes the five *Chlamydia trachomatis* antigens of the first antigen group.) These 13 *Chlamydia trachomatis* antigens form a second antigen group of (1) PepA; (2) LcrE; (3) ArtJ; (4) DnaK; (5) CT398; (6) OmpH-like; (7) L7/L12; (8) OmcA; (9) AtoS; (10) CT547; (11) Eno; (12) HtrA and (13) MurG. These antigens are referred to herein as the 'second antigen group'.

The invention therefore provides a composition comprising a combination of *Chlamydia trachomatis* antigens, said combination selected from the group consisting of two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, or thirteen *Chlamydia trachomatis* antigens of the second antigen group. Preferably, the combination is selected from the group consisting of two, three, four or five *Chlamydia trachomatis* antigens of the second antigen group. Still more preferably, the combination consists of five *Chlamydia trachomatis* antigens of the second antigen group.

Each of the *Chlamydia trachomatis* antigens of the first and second antigen group are described in more detail below.

20 (1) *PepA leucyl aminopeptidase A protein*

One example of a 'PepA' protein is disclosed as SEQ ID NO: 71 & 72 in reference 17 {GenBank accession number: AAC67636, GI:3328437; 'CT045'; SEQ ID NO: 2 below}. It is believed to catalyse the removal of unsubstituted N-terminal amino acids from various polypeptides.

Preferred PepA proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 2; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 2, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These PepA proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 2. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 2. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 2. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

The PepA protein may contain manganese ions.

**SEQ ID NO: 2**

MVLLYSQASWDKRSKADALVLPFWMKNSKAQEAAVVDDEDYKLVYQNALSNSGKKGETAPLPGNDHTKEQKIVLLGLGKSEEVSGTTV  
LEAYAQATTVLRKAKCKTVNILLPTISQLRFSVEEPLTNLAAGVLSLNYYPTYHKVDTSLPFLEKVTVMGIVSKVGDKIFRKEESLF  
EGVYLTRDLVNTNADEVTPKLAVALDLAGEFASLDVKILDRAKAILKBMGLLAVALGAAVEPRFIVLDYQGKPKSKDRTVLIGKG  
VTFDGGGLDLKPGKAMITMKEDMAGAATVLGIFSALASLELPINVGTIIPATENAIGSAAYKMGDVYVGMTGLSVEIGSTDAEGLLIL  
ADAISYALKCNPTRIIDPATLTGAMVVSLLGESVAGFFANNDVLARDLAEASSETGEALWRMPLVEKYDQALHSDIADMKNIGSNRAG  
SITAALFLQRFLEDNPVAWAHLIDIACTAYHEKEELPYPKYATGPGVRCLIHYMBKFLSK

**(2) LcrE low calcium response E protein**

5 One example of a 'LcrE' protein is disclosed as SEQ ID NO<sup>s</sup>: 61 & 62 in reference 17 {GenBank accession number: AAC67680, GI:3328485; 'CT089'; SEQ ID NO: 3 below}.

Preferred LcrE proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 3; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 3, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These LcrE proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 3. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 3. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 3. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

**SEQ ID NO: 3**

MTASGGAGGLGSTQTVVARAQAAAATQDAQEVIQSQEASEASMLKGCEDLINPAAATRIKKGEKFESLEARRKPTADKABKKSEST  
BEKGDTPLEDRPTEDLSEVSGEDFRGLKNSFDDDSSPDEILDALTSPSDPTIKDLALDYLIQTAPSOGKLKSTLIQAKHQQLMSQNPQ  
AIVGGRNVLLASETFASRANTSPSSLRSLYFQVTSSPSNCANLHQMLASYLPSEKTAVMFPLVNGMVADLKSEGPSIPPALKQVYMTE  
LSNLQALHSVNSFPDRNIGNLENSLKHEGHAPIPSLTTGNLTKTPQLVEDKFPSSSKAQKALNELVGPDTGPQTEVLNLFFRALNGC  
SPRIFSGAEKKQQLASVITNTLDAINADNBEDYPKPGDFPRSSFSSTPPHAPVPQSEIPTSPTSTQPPSP

**(3) ArtJ arginine-binding protein**

20 One example of 'ArtJ' protein is disclosed as SEQ ID NO<sup>s</sup>: 105 & 106 in reference 17 {GenBank accession number: AAC67977, GI:3328806; 'CT381'; SEQ ID NO: 6 below}.

Preferred ArtJ proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 6; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 6, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These ArtJ proteins include variants (e.g.

allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 6. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 6. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 6. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

The ArtJ protein may be bound to a small molecule like arginine or another amino acid.

**SEQ ID NO: 6**

MCIKRKKTWIAFLAVVCSFCLTGCLKEGGDSNSKFIIVGTNATYPPPEFVDKRGEVVGFDIDLAREISNLGKTLVDVREFSFDALILNLKQHRIADAVITGMSITPSRLKEILMIPYYGEEIKHLVLVFKGENKHPLPLTQYRSVAVQTGTYQEAYLQLSEVHIRSPDSTLEVLMEVMHGKSPVAVLEPSIAQVVLKDFPALSTATIDLPEDQWVLGYGIGVASDRPALALKIEAAVQBIRKEGVLAELEQKWGLNN

10 **(4) DnaK heat-shock protein 70 (chaperone)**

One example of 'DnaK' protein is disclosed as SEQ ID NO: 107 & 108 in reference 17 {GenBank accession number: AAC67993, GI:3328822; 'CT396'; SEQ ID NO: 7 below}. Other sequences are disclosed in references 18, 19 and 20.

Preferred DnaK proteins for use with the invention comprise an amino acid sequence: (a) having 15 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 7; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 7, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These DnaK proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 7. Preferred 20 fragments of (b) comprise an epitope from SEQ ID NO: 7. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 7. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

25 The DnaK may be phosphorylated e.g. at a threonine or a tyrosine.

**SEQ ID NO: 7**

MSEKRKNKIIGIDLGTTNSCVSVMEGGQPKVIASSEGTRTPSIVAFKGGETLVGIPAKRQAVTNPEKTLASTKRFIGRKFSEVESIKTVPYKVAPNSKGDAVFVDEQKLYTPPEIGAQILMMKETAAYLGETVTEAVITVPAYFNDSQRASKDAGRIAGLDVKRIIPEPTAAALAYGIDKEGDKKIAVFDLGGGTFDISILEIGDGVFEVLSTNGDTLGGDDFDGVIINWMLDBFKKQEGIDLSKDNLALQRLKDAAEKAKIBLSGSSTEINQPFTIDANGPKHLALTTRAQFEHLASSLIERTKQPCQAQALKDAKLSASDIDDVLLVGGMSRMPAVQAVVKEIFGKEPNKGVNPDEVVAIGAAIQGGVLGGEVKDVLLDVIPLSLGIETLGGVMTPLVERNTTIPTQKKQIFSTAADNQPAVTIVVLQGERPMADNKIEGRFDLTDIIPPAPRGHPQIEVTFDIDANGILHVSAKDAASGREQKIRIEASSGLKEDEIQQMIRDAELHKEBDKQRKEASDVKNEADGMIFRABKAVKDYHDKIPABEVKEIEEHIEKVRQAIKEDASTTAIKAASDELSTHMQKIGEAMQAQSASAASSAANAQGGPNINSEDLKKHSFSTRPPAGGSASSTDNIEDADVEIVDKPE

**(5) CT398 protein**

One example of 'CT398' protein is disclosed as SEQ ID NO<sup>s</sup>: 111 & 112 in reference 17 {GenBank accession number: AAC67995, GI:3328825; SEQ ID NO: 8 below}.

Preferred CT398 proteins for use with the invention comprise an amino acid sequence: (a) having 5 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 8; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 8, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These CT398 proteins include variants 10 (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 8. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 8. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 8. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

**15 SEQ ID NO: 8**

MHDALQSILAIQELDIKMRVKKHQNELAKIQALKTDIIRRKVEEKEQEMBKLDQIKGGEKRIQEISDQINKLENQQAAVKKMD  
EFNALTQRMTAANKERRTLEHQLSDLMDKQAGSEDLLISLKESLSSTENSSAIEBEIRBNIRKINEBGRSLLSQRTQLKETTDPELF  
SIYERLLNNKKDRVVVPIENRVCSCGHIALTPQHENLVRKQDHGVFCBHCSDRILYWQBLQSPSAEGATTKRRRRRTAV

**(6) OmpH-like outer membrane protein**

One example of 'OmpH-like' protein is disclosed as SEQ ID NO<sup>s</sup>: 57 & 58 in reference 17 {GenBank accession number: AAC67835, GI:3328652; 'CT242'; SEQ ID NO: 4 below}. A variant 20 sequence is disclosed in reference 21.

Preferred OmpH-like proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 4; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 4, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These OmpH-like proteins include 25 variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 4. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 4. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more; preferably 19 or 30 more, to remove the signal peptide) from the N-terminus of SEQ ID NO: 4. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide as described above, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

**SEQ ID NO: 4**

MKKFLLSLMSLSSLPTFAANSTGTIGIVNLRRCLEESALGKESASPEKMKNQPSNSMGKMEELSSIYSKLQDDDMEGLSETAAA  
ELRKKFEDLSABYNTAQGQYYQILNQSNLKRMQKIMEEVKKASETVRIQEGLSVLNEDIVLSIDSSADKTDAVIKVLDASFQNN

**(7) L7/L12 ribosomal protein**

One example of 'L7/L12' protein is deposited in GenBank under accession number AAC67909

5 (GI:3328733; 'CT316'; SEQ ID NO: 5 below).

Preferred L7/L12 proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 5; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 5, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 10 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These L7/L12 proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 5. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 5. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ 15 ID NO: 5. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

The L7/L12 protein may be N-terminally modified.

**SEQ ID NO: 5**

MTTESLETLVQLSGLTVLELSQLKKLLEEKWDVTAAAPVVAVAGAAAAGDAPASAEPTEFAVILEDVPSDKKIGVLKVVRVTGLAL  
KRAKEMTEGLPKTVKEKTSKSDAEDTVKKLQEAGAKAVAKGL

20 (8) *OmcA cysteine-rich lipoprotein*

One example of 'OmcA' protein is disclosed as SEQ ID NO's: 127 & 128 in reference 17 {GenBank accession number: AAC68043, GI:3328876; 'CT444', 'Omp2A', 'Omp3'; SEQ ID NO: 9 below}. A variant sequence is disclosed in reference 22.

Preferred OmcA proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 9; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 9, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These OmcA proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 9. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 9. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one 30

or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more; preferably 18 or more to remove the signal peptide) from the N-terminus of SEQ ID NO: 9. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide as described above, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

5 The protein may be lipidated (e.g. by a *N*-acyl diglyceride), and may thus have a N-terminal cysteine.

**SEQ ID NO: 9**

MKKTALLAALCSVVSLSSCCRIVDCCPEDIQCSPECESKKDVGGCNSCNGYVPACKPCGGDTHQDAKHGPQARGIPVDGKCRQ

**(9) AtoS two-component regulatory system sensor histidine kinase protein**

One example of 'AtoS' protein is disclosed as SEQ ID NO<sup>s</sup>: 129 & 130 in reference 17 {GenBank 10 accession number: AAC68067, GI:3328901; 'CT467'; SEQ ID NO: 10 below}.

Preferred AtoS proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 10; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 10, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 15 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These AtoS proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 10. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 10. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID 20 NO: 10. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

**SEQ ID NO: 10**

MPKIDTCDSNTTELLAIRTRVTQSYNEAQTISSIPDGIFLLSESGEILICNPQARAILGIPEEDIQLVTRMPHDFFPDTFPGFSVQ EALEKEVPPKTIRLTLSQELSQKEVEVFVRKNISHDFLFLIRDRSDYRQLEQAIEKYRSISELGKIAATLAHEIRNPLTSISGFATL LKEELSSERHQRMNVIEGTRSLNSLVSSMLEYTKIQPLNRLSIDLQDFSSLIPELSLTFPSCTFRRTILSPIQRSIDPDRLRCVI WNLVKNAVEASDEEIPLELHEKGFSINTGTLPPNIQEKLFIPIFFTTPKPQGNGLGLAEAHKIMRLHGGDLVVSTQDNRTTFTILWTPA

**(10) CT547 protein**

25 One example of 'CT547' protein is disclosed as SEQ ID NO<sup>s</sup>: 151 & 152 in reference 17 {GenBank accession number: AAC67995, GI:3328825; SEQ ID NO: 11 below}.

Preferred CT547 proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 11; and/or (b) which is a fragment of at least

*n* consecutive amino acids of SEQ ID NO: 11, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These CT547 proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 11. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 11. Other preferred fragments lack 5 one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 11. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

10 **SEQ ID NO: 11**

MKVILRALCLFLVLPCCYARVPSFEPFRGAIAPNRYTPKHSPELYFEMGDKYFQAKKFQALLCFGMITHHFPEHALHPKAQFLVGL  
CYLEMGHPDLAQKALTQYQELADTEYSEQLFAIKYSIAQSFANGRKKNIVPLBGFPKLLKADTDALRIFEEIVTASSDADLKASALYA  
KGALLFDRKEYSEAIKTLKKVSLQFPSHSLSPESFTLIAKIHCLQALQEPYNBQYLQDARMNAAALRKQHPNHPNSNTEVENYIHHMCA  
AYASCLYSTGRFYEKRKASSAKIYYSIALENFPDTSYVAKCNKRLERLSKQMS

**(11) Enolase (2-phosphoglycerate dehydratase) protein**

One example of an 'Eno' protein is disclosed as SEQ ID NO<sup>s</sup>: 189 & 190 in reference 17 {GenBank accession number: AAC68189, GI:3329030; 'CT587'; SEQ ID NO: 12 below}.

15 Preferred Eno proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 12; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 12, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These Eno proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 12. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 12. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 12. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, 20 of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

25 The Eno protein may contain magnesium ions, and may be in the form of a homodimer.

**SEQ ID NO: 12**

MFDVVISDIEAREILDGYPTLCVKVITNTGTFGEACVPSGASTGIKEALELRDKDPKRYQGKGVLQAISNVKVLMPALQGFSVFD  
QITADAIMIDADGTPNKEKLGANAILGVSLALAKAAANTLQRPLYRLGGSPSHVLPCPMMNLINGGMHATNGLQFQEFMIRPISAPS  
LTEAVRMGAEVFNALKKILQRQLATGVGDEGGFAPNLASNAEALDLITAIETAGFTPREDISLALDCAASSFYNTQDKTYDGKSYA  
DQVGILAELEHYPIDSIEDGLAEDFEGWKLLSETLGDRVQLVGDLLFVTNSALIAEGIAQGLANAVLIKPNQIGTLTETAEAIRLA  
TIQGYATILSHRSGETEDTTIADLAVAFNTGQIKTGSLSRSERIAKYNRLMAIEBEMGPEALFQDSNPFSA

**(12) HrtA DO protease protein**

One example of an 'HrtA' protein is disclosed as SEQ ID NO<sup>s</sup>: 229 & 230 in reference 17 {GenBank accession number: AAC68420, GI:3329293; 'CT823'; SEQ ID NO: 13 below}.

Preferred HrtA proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 13; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 13, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These HrtA proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 13. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 13. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more; preferably at least 16 to remove the signal peptide) from the N-terminus of SEQ ID NO: 13. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide as described above, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain). In relation to SEQ ID NO: 13, distinct domains are residues: 1-16; 17-497; 128-289; 290-381; 394-485; and 394-497.

**SEQ ID NO: 13**

MMKRLLCVLLSTSVFSSPMIGYSASKKDSKADICLAVSSGDQEVSQEDLLKEVSRGFSRVAAKATPGVYYIENFPKTGNQAIASPGNK  
RGFQENPDFYFNDEFPNRFFGLPSHREQQRPQQRDAVRGTGFIVSEDGYVVTNHHVEDAGKIHVTIHDGQKYTAKIVGLDPKTDLAV  
IKIQAELPKFLTPGNSDQLQIGDWAIAIGNPFGQLQATVTGVVISAKGRNQLHIVDFEDFIQTDAAINPGNSGGPLLNINGQVIGVNTA  
IVSGSGGYIGIGFAIPSLMAKRVIDQLISDGQVTRGFLGVTLQPIDSBLATCYKLEKVY GALVTDVVKGSPAEKAGLRQEDVIVAYNG  
KEVESLSALRNAISLMMPGTRVVLKIVREGKTIEIPVTVTQIPTEDGVSA LQKMGVRVQNITPEICKKLGAA DTRGILVVAVEAGSP  
AASAGVAPGQLILAVNRQRVASV BELNQVLKNSKGENVLLMVSQGDVVRPIVLKSDE

**(13) MurG peptidoglycan transferase protein**

20 One example of a 'MurG' protein is disclosed as SEQ ID NO<sup>s</sup>: 217 & 218 in reference 17 {GenBank accession number: AAC68356, GI:3329223; 'CT761'; SEQ ID NO: 14 below} It is a UDP-N-acetylglucosamine-N-acetyl muramyl-(pentapeptide)pyrophosphoryl-undecaprenol N-acetylglucosamine transferase.

Preferred MurG proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 14; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 14, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These MurG proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 14. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 14. Other preferred fragments lack one or

more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 14. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide as described above, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain). The MurG may be lipidated e.g. with undecaprenyl.

**SEQ ID NO: 14**

MKKINKIVLAVGGTGGHIIPALAARETFIHEDIEVLLLKGGLAHFLGDDSEVAYCDIPSGSPFSLRVNRMPGAKQLYKGYVAALQKI  
RDPTPDLAIGFGSYHSLPAMLASIRSRIPLFLHQQNIVPGKVNLPSRFAKGVGMSFAAGEHFHCRAEEVFLPIRKLSSEQIVFPGAS  
PVICVVGGSQGAKILNDVVPKALARIRESYSNLYVHHIVGPKGDLQAVSQVYQDAGINHTVTAFDHMLGVLQASDLVISRSGATMLN  
ELLWVQVPAILIPYPGAYGHQEVDNAKFFTHTVGGGTMILQKYLTERSLSKQVLLALDPATSENRRKAMLSAQQQKSFKSLYQFICESL

The immunogenicity of other known *Chlamydia trachomatis* antigens may be improved by combination with two or more *Chlamydia trachomatis* antigens from either the first antigen group or 10 the second antigen group. Such other known *Chlamydia trachomatis* antigens include a third antigen group consisting of (1) PGP3, (2) one or more PMP, (3) MOMP (CT681), (4) Cap1 (CTS29); (5) GroEL-like hsp60 protein (Omp2); and (6) 60 kDa Cysteine rich protein (omcB). These antigens are referred to herein as the “third antigen group”.

The invention thus includes a composition comprising a combination of *Chlamydia trachomatis* 15 antigens, said combination selected from the group consisting of two, three, four, or five *Chlamydia trachomatis* antigens of the first antigen group and one, two, three, four, five or six *Chlamydia trachomatis* antigens of the third antigen group. Preferably, the combination is selected from the group consisting of three, four, or five *Chlamydia trachomatis* antigens from the first antigen group and three, four, or five *Chlamydia trachomatis* antigens from the third antigen group. Still more 20 preferably, the combination consists of five *Chlamydia trachomatis* antigens from the first antigen group and three, four or five *Chlamydia trachomatis* antigens from the third antigen group.

The invention further includes a composition comprising a combination of *Chlamydia trachomatis* 25 antigens, said combination selected from the group consisting of two, three, four, five, six, seven, eight, nine, ten, eleven, twelve or thirteen *Chlamydia trachomatis* antigens of the second antigen group and one, two, three, four, five or six *Chlamydia trachomatis* antigens of the third antigen group. Preferably, the combination is selected from the group consisting of three, four, or five *Chlamydia trachomatis* antigens from the second antigen group and three, four or five *Chlamydia trachomatis* from the third antigen group. Still more preferably, the combination consists of five 30 *Chlamydia trachomatis* antigens from the second antigen group and three, four or five *Chlamydia trachomatis* antigens of the third antigen group.

In either of the above combinations, preferably the *Chlamydia trachomatis* antigens from the third antigen group include Cap 1. Or, alternatively, in either of the above combinations, preferably the *Chlamydia trachomatis* antigens from the third antigen group include MOMP.

Each of the *Chlamydia trachomatis* antigens of the third antigen group are described in more detail  
5 below.

**(1) Plasmid Encoded Protein (PGP3)**

One example of PGP3 sequence is disclosed in, for example, at Genbank entry GI 121541. Immunization with pgp3 is discussed in Ref. 23 and 24. One example of a PGP3 protein is set forth below as SEQ ID NO: 15.

10 Preferred PGP3 proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 15; and/or (b) which is a fragment of at least  $n$  consecutive amino acids of SEQ ID NO: 15, wherein  $n$  is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These PGP3 proteins include variants  
15 (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 15. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 15. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ  
20 ID NO: 15. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

**SEQ ID NO: 15**

MGNSGFYLYNTQNCVFADNIKVGQMTEPLKDDQIILGTTSTPVAAKMTASDGISLTVSNNPSTNASITIGLDAEKAY  
QLILEKLGDQILGGIADTIVDSTVQDILDKITTDPSLGLLKAFNNFPITNQICNGLFTPRNIETLLGGTEIGKFTV  
TPKSSGSMFLVSADIIASRMEGGVVLALVREGDSKPYAISYGYSSGVNLCSRTRINTGLPTTYSLRVGGLESG  
25 VVVVNALSNGNDILGITNTSNVSFLEVIPQTNA

**(2) Polymorphic Membrane Proteins (PMP)**

A family of nine *Chlamydia trachomatis* genes encoding predicted polymorphic membrane proteins (PMP) have been identified (*pmpA* to *pmpJ*). See Ref. 25, specifically Figure 1. Examples of Amino  
30 acid sequences of the PMP genes are set forth as SEQ ID NOS: 16 – 24. (These sequences can also be found at Genbank Ref. Nos. GI 15605137 (*pmpA*), 15605138 (*pmpB*), 15605139 (*pmpC*), 15605546 (*pmpD*), 15605605 (*pmpE*), 15605606 (*pmpF*), 15605607 (*pmpG*), 15605608 (*pmpH*), and 15605610 (*pmpI*)). These PMP genes encode relatively large proteins (90 to 187 kDa in mass). The majority of these PMP proteins are predicted to be outer membrane proteins, and are thus also referred to as Predicted Outer Membrane Proteins. As used herein, PMP refers to one or more of the  
35

*Chlamydia trachomatis* pmp proteins (*pmpA* to *pmpI*) or an immunogenic fragment thereof. Preferably, the PMP protein used in the invention is *pmpE* or *pmpI*. Preferably, the PMP protein used in the invention comprises one or more of the fragments of *pmpE* or *pmpI* identified in International Patent Application PCT/US01/30345 (WO 02/28998) in Table 1 on page 20 (preferred fragments of *pmpE*) or Table 2 on page 21 (preferred fragments of *pmpI*).

Preferred PMP proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to one of the polypeptide sequences set forth as SEQ ID NOS: 16 - 24; and/or (b) which is a fragment of at least *n* consecutive amino acids of one of the polypeptide sequences set forth as SEQ ID NOS: 16 - 24, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These PMP proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of the polypeptide sequences set forth as SEQ ID NOS: 16 - 24. Preferred fragments of (b) comprise an epitope from one of the polypeptide sequences set forth as SEQ ID NOS: 16 - 24. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of one of the polypeptide sequences set forth as SEQ ID NOS: 16 - 24. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

20 **SEQ ID NO: 16 (*pmpA*)**

MNRVIEIHAHYDQRQLSQSPNTNFLVHHPYLTLPKFLLGALIVYAPYSFAEMELAISGHKQGKDRDTFT  
MISSCPEGTNYIINRKLILSDFSLLNKVSSGGAFRNLAKGISPLGKNSSASIHFKHININGFGAGVFSES  
SIEFTDLRKLVAFGSESTGGIFTAKEDISFKNNHHIAFRNNNITKGNGGV1QLQGDMKGSVSFVDQRGAI  
FINNQAVTSSSMKHSGRGGAISGDFAGSRILFLNNQQITFEGNSAVHGGAIYNKNGLVEFLGNAGPLAFK  
15 ENTTIANGGAIYTSNFKANQQTSPILFSQNHANKGGAIYAQYVNLEQNQDTIRFEKNTAKEGGGAITSS  
QCSITAHTIIIPSDNAAGDLGGGAILLEGKKPSLTIAHSGNIAFSGNTMLHITKKASLDRHNSILIKEA  
PYKIQLAANKNHSIHFFDPVMALSASSSPIQINAPEYETPFFSPKGIVFSGANLDDAREDVANTSIF  
NQPVHLYNGTLSIENGHLIVQSFQTKTGGRISLSPGSSLALYTMSFFHGNISSKEPLEINGLSFGVDIS  
PSNLQAEIRAGNAPRLSGSPSIHDPEGLFYENRTAASPQMEILLTSDKIVDISKPTTDLSVTNKQSG  
30 FQGAWHFSWQPNTINNTKQKILRASWLPTEGYVLESNRVGRAPVNSLWSTFLQLTASHNLGDHLCNNRS  
LIPTSYFGVLIGGTGAEMSTSSEEESFISRLGATGTSIIRLTPSLTLSGGGSHMFGDSFVADLPEHITS  
EGIVQNVGLTHYWGPLTVNSTLCAALDHNMVRICSKKDHTYWKWDTFGMRGTLGASYTFLEYDQTMRVF  
SFANIEATNILQRAFETGYNPRFSKTKLLNIAPIGIGYEFLGNSSFALLGKGSIGYSRDIKRENPS  
TLAHLAMNDFAWTNGCSVPTSAHTLANQLILRYKACSLYITAYTINREGKNLSNSLSCGGYVGF

35 **SEQ ID NO: 17 (*pmpB*)**

MKWLSATAVFAAVLPSVSGFCPPPEPKELNFSRVGTSSSTFTETVGEAGAEYIVSGNASFTKFTNIPPTD  
TTTPTNSNSSSSNGETAVSEDSDTTTPDPKGGAFYNAHSGVLSFMTRSGTEGSLTLSEIKITGE  
40 AIFSQGELLFTDLTGLTIQNNLSQLSGGAIFGESTISLSGITKATFSSNSAEVPAPVKKPTEPKAQTASE  
TSGSSSSSGNDVSSPSSSRAEPAAANLQSHFICATATPAAQTDETSTPSHKPGSGGAIYAKGDLTIAD  
SQEVLFINSINKATKDGGIAFAEKDVSFENITSLKVQTNGAEBKGGAIYAKGDLSIQSSKQSLFNSNYSKQG  
GGALYVEGDINFQDLBEIRIKYKAGTFETKKITLPKAQASAGNADAWASSSPQSGSGATTVSNSGDSSS  
GSDSDTSETVPATAKGGGLYTDKNLISITNITGIIBIANNKATDVGGGAYVKTLCENSRLQFLKNSSD  
KQGGGIYGEDNITLSNLTGKTLFQENTAKEEGGGLFIKGTDKALTMTGLDSFCLINNTSEKGGGAFVTK  
EISQTYTSDVETIPGITPVHGETVITGNKSTGGNGGGVCTKRLALSNLQSIISGNSAAENGGAHTCPD

SFPTADIAEQPAAASAATSTPESAPVUSTALSTPSSSTVSSLTLLAASSQASPATSNKETQDPNADTDLL  
IDYVVDTTISKNTAKGGGIYAKKAKMSRIDQLNISENSATEIGGGICCKESLELDALVSLSVTENLVGK  
EGGLHAKTVNISNLKGFSFSNNKANSSTGVATTASAPAAAASLQAAAAPSSPATPTYSGVVGGA  
IYGEKVFSQCCTCQFSGNQAIIDNNPSQSSLNVQGGAIYAKTSLSIGSSDAGTSYIFSGNSVSTGKSQT  
5 TGQIAGGAIYSPTVLNCPATFSNNTASMATPKTSSEDGSSGNSIKDTIGGAIAGTAITLSGVSRFGNT  
ADLGAAIGTLANANTPSATSGSQNSITEKITLENGSFIFERNQANKRGAIYSPSVSIKGNNITFNQNTST  
HDGSAIYFTKDATIESLGSVLFITGNVTATQASSATSGQNTNTANYGAIYGDPGTTQSSQTDAILLLA  
SSGNITFSNNSLQNNQGDTASKFCIAGYVKLSLQAAGKTIISFFDCVHTSTKKIGSTQNVTETLDINK  
EENSNPYTGTIVFSSSELHENKSYIPQNAILHNGLVKEKTELHVVSFEQKEGSKLIMKPGAVLSNQNI  
10 NGALVINGLTIDLSSMGTPOAGEIFSPPELIVATTSSASGGSGVSSIPTNPKRISAAPSGSAATTPT  
MSENKVFLTGDLTLIDPNFQNPMLGSDLDVPLIKLPTNTSDVQVYDLTLSGDLFPQKGYMGWTLD  
NPQTGKLQARWTFDTYRRWVYIPRDNHFYANSILGSQNSMIVVKQGLINNMLNARFDDIAYNNFWVSGV  
GTFLAQGQGPLSEEFSYRSRTVAIDAKPRQDFILGAAFSKMVGKTKAIKKMHNYFKGSESYQASVY  
GGKFLYFLNKHQHGWLPLIQGVVSYGHIKHDTTLYPSIHERNKGWDWDLGLWADRISMDLKEPSKD  
15 SSKRITVYGELEYSSIRQKQFTEIDYDPRHFDCAYRNLSLPVGCAVEGAIMNCNILMYNKLALAYMPSI  
YRNNPVCKYRVLSSNEAGQVICGVPTRTSARAESTQLYLGPFWTLYGNYTIDVGMYTLSQMTSCGARMI  
F

**SEQ ID NO: 18 (pmpC)**

MKFMSATAVFAAALSSVTEASSIQDQIKNTDCNVSKLGYSTSQFTDMMLADNTEYRAADSVSFYDFSTS  
20 SRLPRKHLSSSSEAASPTEGVSSSSGETDEKTEEELDNGGIYAREKLTISESQDSLSNQSIELHDNSI  
PPGEGEVIFDHVALKNGGAIYGEKEVVFENIKSLLVEVNIAVEKGGSYAKERSLENVTEATFSSNGG  
EQGGGGIYSEQDMLISDCNNVHFQGNAAGATAVKQCLDBEMIVLLAEVDLSEDLDSTPETEQTESNG  
NQDGSSSETDTQVSESPESTPSDDVLKGGGIYTEKSLTITGITDIFVSNIAITDGGAVFTKENLSC  
TNTNSLQFLKNSAGQHGGGAYVTQTMVTNTSESITPPLIGEVIFSENTAKGGGICTNKLSSLNLK  
25 TVTLTKNSAKESGGAIYFTDLASIPISTDTPESSTPSSSSPASTPEVVASAKINRFFASTAKPAAPSLTEAE  
SDQTDQTESTDNTNSIDVSIENILNVAIQNNTSAKGGAIYGGKALESRINNLELSGNSSQDVGGCLCT  
ESVEFDAIGSLLSHYNSAAKEGGAIHSKTVTLSNLKSTFTFADNTVKAIVESTPEAPEEIPPVEGEESTA  
TEDPNSNTEGSSANTNLEGSQDTADTGTGDVNNEQDTSVTGNAESEEQLQDSTSNEENTLPNSNIDQ  
SNENTDESSDSHTEITDESVSSSSESGSSTPDQDGGAAASSGAPSGDQSI SANACLAKSYAASTDSSPVSN  
30 SSGSEEPVTSSSDSDVTASSNDPSSSSGDSAGDSEEPTPEAGSTTETLTLIGGAIYGETVKIENFSG  
QGIFSGNKAIDNTTEGSSSKSDVLGAVYAKTLFNLDGSSRRTVTSGNTVSSQSTTQVAGGAIYSPT  
VTIATPVVFSKNSATNNANNTDTQRKDTFGCAIGATSAVSLSGGAHLENVADLGSAILGLVPGTQNTET  
VKLESGSYYFEKNKALKRATIYAPVSIKAYTATFNQNRSLEEGSAIYFTKEASIESLGSVLFGNLVT  
TLSTTTEGTATTSGDVTKYGAAIFGQIASSNGSQTDNLPLKLIASGGNICFRNEYRPTSSDTGTSTFC  
35 SIAGDVKLTMQAAGKTISFFDAIRSTKKTGTQATAYDTLDINKSEDSETVNSAFTGTILFSSSELHENK  
SYIPQNVVLHGSGLVLPNTTELHVISFEQKEGSSLVMPGSQLNQTVADGALVINNMIDLSSVEKNGI  
AEGNIFTPPPELRIIDTTGGGGTPSTDSESNQNSDDTEEEQNNNDASNQGESANGSSPAVAAHTSRTR  
NFAAAATATPTTTPTATTTSNQVILGGEIKLIDPNFTFFQNPALRSDQQISLLVLPDSSKMQAQKIVL  
TGDIAPQKGYTGLTLDPDQLQNGTISVWLWKFDSYRQWAYVPRDNHFYANSILGSQMLMVTVKQGLNDK  
40 MNLARFEVSYNNLWISGLGTMISQVGTPTSEEFTYYSRGASVALDAKPAHDVIVGAAPSKMIGTKSLK  
RENNYTHKGSEYSYQASVYGGKPFHVINKKTEKSLPLLQGVISYGYIKHDTVTHYPTIRERNKGEWED  
LGWLTALRVSSVLRTPAQGDTKRITVYGELEYSSIRQKQFTEYEPRYFDNCTYRNLAIPMGLAFEGEL  
SGNDILMYNRFSVAYMLSIRNSPTCKYQVLSSEGGEIIICGVPTRNSARGEYSTQLYLGPLWTLYGSYT  
IEADAHTLAHMNCGARMTF  
45

**SEQ ID NO: 19 (pmpD)**

MSSEKDIKSTCSKPSLSVAAILASVGLASCVDLHAGGQSVNELVYVGPQAVLLLQIRDLFVGSKDSQ  
AEGQYRLIVGDPSSFQEKDADTLPGKVBQSTLFSVTNPVVFQGVQDQDQVSSQGLICSFSSNLDS PRDG  
50 ESFLGIAFVGDSSKAGITLTDVKASLSGAALYSTEDLIFEKIKGGLEFASCSSLEQGGACAAQSILIHDC  
QGLQVKHCTTAVNAEGSSANDHLGFCCGAFVTGSLSGEKSILYMPAGDMVVANCDGAI SPEGNSANFANG  
GAIAASGKLFVANDKTSFIENRALSGGAI AASSDIAFQNCAELVFKGNCAIGTEDKGSLGGAISSLG  
TVLLQGNHGTCDKNESASQGGAI FGKNCQISIDNEGPVVFRDSTA CLGGGAI AAQEIVSIQNNQAGISFE  
GGKASFGGGIACGSFSSAGGASVLTIDISKNLGAISFSRTLCTTS DLQMEYQGGGALFGENISLSENA  
GVLTFKDNIVKTFASNGKILGGGAI LATGKVEITNNSEGISFTGNARAPQALPTQEEFPLFSKKEGRPLS  
55 SGYSGGGAILGREVAILHNAAVVFEQNRLQCSEEBATLLGCCGGAVHGMSTSIVGNSSVRFGNNYAMG  
QGVSGGALLSKTVQLAGNGSVDFSRNIASLGGGALQASEGNCELVDNGYVLFRDNRGVYGGAI SCLRGD  
VVISGNKGRVEFKDNIATRLYVEETVEKVEEVEPAPEQKDNNELSFLGRAEQSFITAANQALFASBDGDL

SPESSI SSEEELAKRRECAGGAIFAKRVRIVDNQEAVVFSNNFSDIYGGAI FTGSLREEDKLDGQI PEVLI  
SGNAGDVVFSGNSKRDEHLPTHCGGAICTQNLTISQNTGNVLFYNNAVCSGGAVRIEDHGNVLLEAFGG  
DIVFKGNSSFRAQGSDAIYFAGKESHITALNATEGHIAVFHDALVENLEERKSAEVLLINSRENPGYTG  
SIRFLEAESKVPCIHQQGSLELLNGATLCSYGFQDAGAKLVLAAAGAKLKILDSTPVQQGHAISKPE  
5 ABIESSSEPEGAHSLWIAKNAQTTVPMVDIHTISVDLASFSSSQEGTVEAPQVIVPGGSYVRSGELNLE  
LVNTTGTYENHALLKNEAKVPLMSFVASGDEASAEISNLVSVDLQIHVVTPEIEEDTYGHMGDWSEAKI  
QDGTLVISWNPTGYRLDPQKAGALVFNALWEEGAVLSALKNARFAHNLTAAQRMEPDYSTNVWGFAFGGFR  
TLSAENLVAIDGYKGAYGGASAGVDIQLMEDFVLGVSGAAFGLKMDSQKFDAEVSRKGVGSVTGFLAG  
10 SWFFKGQYSLGETQNDMKTRYGVLGESSASWTSGVLADALVEYRSLVGPVRPTFYALHFNPYEVSYAS  
MKFPGFTEQGREARSFEDASLTNITIPLGMKFELAFIKGQFSEVNSLGISYAWEAYRKVEGGAVQLLEAG  
FDWEGAPMDLPRQELRVALENNTWESSIONSYFSTVLGLTAFCCGFTSTDASKLGYEANTGLRLIF

**SEQ ID NO: 20 (pmpE)**

MKKAFFFLIGNSLGLAREVPSRIFLMPNSVPDPTKESLSNKISLTGDTHNLTCYLDNLRYILAILQK  
TPNEGAATITDYLSFFDTQKEGIYFAKNLTPESGGAIYGASPNSPTVEIRDIGPVIFENNCCRIFTW  
15 RNPYAADKIREGGAIHAQONLYINHNHDVVGFMKNFSYVQGGAISTANTFVSENQSCFLMDNICIQTNT  
AGKGGAIYAGTSNSFESNNCDLFFINNACCAGGAIIFSPICSLTGNRGNIVFYNNRFCFKNVENTASSEASDG  
GAIKVTRLDVTGNRGRIFPSDNITKNYGGAIYAPVVTLVDNGPTYFINNIANNKGAIYIDGTSNSKIS  
ADRHAIIFNENIVTNVTNANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLIFYDPIEVSNAGSVSF  
20 NKEADQTGSVVFSGATVNSADFHQRNQTKTPAPLTLNGFLCIEDHAQLTVNRFTQTGGVVSILNGAVL  
SCYKNGTGDASNASITLKHIGLNLSILKSGAEIPLLWVEPTNNNNYTAADTAATFSLSDVKLSLIDDY  
GNSPYESTDLTHALSSQPMLSISEASDNQLQSENIDFSGLNVPHGWQGLWTWGWAKTQDPEPASSATIT  
DPQKANRFHRTLLLTLWPAGYVPSPKHRSPLIANTLWGNMLLATESLKNSAELTPSGHPFWGITGGGLGM  
MIVYQDPRENHPGFHMRSSSGYSAGMIAGQHTFSLKSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEG  
25 FLLTKLVGLYSYGDHNCHHFYTQGENLTSQGTPRSQTMGGAVFPDLPMKPFGSTHILTAPFLGALGISS  
LSHFTBEVGAYPRSFSTKTPLINVLVPIGVKGSMNATHRPQAWTVELAYQPVLYRQEPGIAAQQLASKGI  
WFGSGSPSSRHAMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRP

**SEQ ID NO: 21 (pmpF)**

MIKRTSLSPACLSFFYLSTISILOQANETDTLQFRRFTFSDREIQFVLDPASLITAQNIVLSNLQSNGTGA  
CTISGNTQIQFSNSVNTTADSGGAFDMVTTSPASDNANLLFCNNYCTHNKGGAIRSGGPIRFLNNQD  
30 VLFYNNISAGAKYVGTGDHNBNRGGALYATTITLTGNRTLAFINNMSGDCGGAISADTQISITDTVKGI  
LFENNHTLNHIPTYTQAENMARGGAI CSRRDLCISNNSGPIVFYNQNQGGKGGAISATRCVIDNNKERIIF  
SNNSSLGWSQSSASNGGAIQTTQGFTLRNNKGSIYFDSNTATHAGGAINCYIDIRDNGPVYFLNNSA  
WGAANLNSKPRSATNYIHTGTGDIVFNNNNVFTLDGNLLGKRKLPHINNNBEITPYTSLGAKKDTRIYPY  
DLFQWERVKENTSNNPPSPTSRNTITVNPETEFGAVVFSYNQMSDIRTLMGKEHNYIKEAPTTLKFGT  
35 LAIEDDAELEIFNIPFTQNPSTSLLALGSGATLTGKHGKLNITNLGVILPIILKEGKSPPCIRVNPQDMT  
QNTGTQTPSSTSSISTPMIIFNGRLSIVDENYESVYDSMDLSRGKAEQLILSIETTNDQLDNSWQSSL  
NTSLLSPPHYGYQGLWTPNWITTTYTITLNNNNSAPTSATSIAEQKKTSETFTPSNTTASIPNIKASAG  
SGSGSASNSGEVTITKHTLUVNWAPVGYIVDPIRRGDLIANSLVHSGRNMTMGLRSLLPDNSWPALQGAA  
40 TTLFTKQQKRLSYHGSSASKGYTVSSQASGAHKFLSFSQSSDKMKEETNNRLSSRYYLSALCFEH  
PMFDRIALIGAACNYGTHNMRSFYGTKKSSKGKFHSTLGAISLRCELRDSMPLRSIMLTPFAQALFSRT  
EPASIRESGDLARLFTLEQAHTAVVSPIGIKGAYSSDTWPTLSWEMELAYQPTLYWKRPLLNTLIQNN  
SWVTNTPLAKHSFYGRGSHSLKFSLKLFANYQAEVATSTVSHYINAGGALVF

**SEQ ID NO: 22 (pmpG)**

45 MQTSHKFFLSMILAYSCCSLSGGGYAAEIMIPQGIYDGETLTFSFPTVIGDPSGTTVFSAGELTKLNL  
DNSIAALPLSCFGNLLGSFTVLGRGHSLTFENIRTSTNGAALSDSANGLFTIEGFKELSFSNCNSLLAV  
LPAATTNNGSQTPTTSTPSNGTIYSKTDLLNNNEKFSFYSNLVSGDGGAI DAKSLTVQGISKLCVFQE  
NTAQADGGACQVVTFSAMANEAPIAFIANVAGVRGGGIAAVQDGQQGVSSSTSTEDPVVSFSRNTAVEP  
DGNVARVGGGIYSYGNVAFLNNNGKTLFLNNVASPVYIAAEQPTNGQASNTSDNYGDGGAI FCKNGAQAG  
50 SNNSGVSFDGEGVVFSSNVAAGKGGAIAKKLSVANC GPVQFLGNIANDGGAIYLGESGELSADYG  
DIIFDGNLKRTAKENAADVNGVTVSSQAIISMGSGKITT LRAKAGHQILFNDPIEMANGNNQPAQSSEPL  
KINDGEGYTGDIVFANGNSTLYQNVTIEQGRIVLREAKL SVNLSQTGGSLYMEAGSTLDFVTPOPPQQ  
PPAANQLITLSNLHLSLLANNAVTPPTNPPA QD SHPAIIGSTTAGSVTISGPPIFEDDDTAYDRY  
DWLGSNQKIDV LKQLGTQPSANAPS DLTGNEMPKYQGSWKLAWDPNTANNGPYTLKATWTKTGYNP  
55 GPERVASLVPNSLWGSILDIRSAHSAIQASVDGRSYCRGLWVSGVSNFYHDRDALGQGYRYISGGYSLG

ANSYFGSSMGLAFTEVFGRSKDYVVCRSNHHACIGSVYLSTKQALCGSYLFGDAFIRASYGFGNQHMKT  
SYTFAEESDVRWDNNCLVGEIGVGLPIVITPSKLYLNELRPFVQAESYADHESFTEEGDQARAFRSGHL  
MNLSVPVGVKFDRCSSTHPNKYSFMGAYICDAYRTISGTQTLSSHQETWTTDAFHLLARHGIVRGSMYA  
SLTSNIEVYGHGRYEYRDTSRGYGLSAGSKVRF

5

**SEQ ID NO: 23 (pmpH)**

MPFSLRSTSFCFLACLCSYSYGFASSPPQVLTPNVITPKGDDVYNGDCAFVNHYAGAENGSIISANGDN  
LTITGQNHTLSFTDSQGPVLQNYAFISAGETLTKDFSSLMF SKNVSCGBKGMSGKTVSISGAGEVIFW  
10 DNSVGYSPLSIVPASTPTPPAPAPAPAASSSLSPVSDARKGSIPS VETSLEISGVKKGVMDNNAGNFG  
TVFRGNNSNNAGSGGSGSATTPSFTVKNCKGKVSDNVASCGGGVVYKGTVLKDNEGGIFFRGN TAYD  
DLGI LAATS RDQNTETGGGGVICS PDDSVK FEGNKGSIVFDYNPAKGRGGSILTKEFSLVADDSSVFSN  
NTAEKGGAIYAPTI DISTNGGSILFERNRAEGGAICVSEASSG STGNLTLASADGDIVFSGNMTSDRP  
GERSAARILSDGTTVSLNASGLSKIFYDPVVQNNSAAGASTPS PSSSSMPGAVTINQSGNGSVIFTAES  
LTPSEKLQVLNSTSNFPGALT VSGGELVVTEGATLTGTTATSGRVTLGSGASLSAVAGAANNYTCTV  
15 SKLGIDLESFLTPNYKTAILGADGTVNSGSTLDLVMESEA EVYDNPLFVGSLTIPFVTLSSSASNGV  
TKNSVTINDADAAYHYQGGSWSADWTKPPLAPDAKGMPV PNTNNTLYLTWRPASNYGEYRLDPQRKGELV  
PNSLWVAGSALRTFTNGLKEHYVS RDVG FVASLHALGDYI LNYTQDDR DGPLARYGGFQATAASHYENG  
IFGVAFGQLYGQT KSRMYYSKDAGNMMLSCFGRSYVDIKGTETV MYWETAYGYSVHRMHTQYFNDKTQK  
20 FDHSKCHWHNNNYYAFVGAEHN FLEYCIPTRQFARDYELTGFMRPEMAGGWSSSTRET GSLTRYFARGSG  
HNMSLPIGIVAHAVSHVRRSPPSKLTNMGYR PDIWRVTPHCNMBIIANGVKTPIQGSPLARHAF FLEVH  
DTLYIHHGRAYMNYSLDARRQTAHFVSMGLNRIF

**SEQ ID NO: 24 (pmpI)**

MRPDHMNFCCCAA ILSSAVLFGQDPLGETALLTKNPNVVCTFFEDCTMESLFPALCAHASQDDPLYV  
25 LGNSYCWFVSKLHITDPKEALFKEKGDSL IQNFRFLSFTDCSSKESSPSIIHQKNGQLSLRNNGSMSFCR  
NHAEGSGGAI SADAFSLQHNYLFTAFEENSSKGNGGAIQ AQTFSLSRN VPISFARNRADLNGGAI CCSN  
LICSGVNPLFFT GNSATNGGAICCISDLNTSEKGSLSLACNQETLFASNSAKEGGAIYAKHMVLRYNG  
PVSFINNSAKIGGAI AIQSGGSL SILAGEGSVLFQNN SQRTSDQGLVRNAIYLEKDAILSSLEARNGDIL  
PPFDPIVQESSSKESPLPSSI QASV TSPTPATASPLVIQTSANRSVIFSSERLSEE EKTPDNLTSQLQOPI  
30 ELKSGRLV LKDRAVLSAPSLSQDPQALLIMEAGTSLKTSIDLK LATLSIPLHSLDTEKSVTIHAPNLSIQ  
KIFLSNSGDENFYENV ELLSKEQNNIPLLTL SKEQSHLHPDGNLSSHFGYQGDWTF SWKDSDEGHSLIA  
NWTPKNYVPHPERQSTLVANTLWNTYSDMQAVQSMINTIAHGGAYLFGTWGSAVSNLFYAH DSSGKPIDN  
WHHRSLG YLFGISTHS LDDHSFCLAAGQLLGKSSDSFITSTETTSYIATVQAQLATPLMKISAQACYNES  
IHELKTKYRSFSKEFGFSWHSV AVS GEVCASIPIVSNGSGLFSSFSIFS KLQGFSGTQDGFEESSGEIRS  
35 FSASSFRNISLPMGITFEKKSQKTRNYYFLGAYIQDLKRDVESGPVLLK NAVSWDAPMANLDSRAYMF  
RLTNQRALHRLQTL NVSYVLRGQSHSYSLDLGITYRF

**(3) Major Outer Membrane Protein (MOMP) (CT681)**

One example of a MOMP sequence is disclosed as SEQ ID NOS 155 and 156 in International Patent  
40 Application No. PCT/IB02/05761 (WO 03/049762). The polypeptide sequence encoding MOMP is  
set forth below as SEQ ID NO: 25. This protein is thought to function *in vivo* as a porin {ref. 26},  
and to be present during the whole life cycle of the bacteria {ref. 27}. MOMP displays four variable  
domains (VD) surrounded by five constant regions that are highly conserved among serovars {ref. 28  
29}. *In vitro* and *in vivo* neutralizing B-cell epitopes have been mapped on VDs {Ref. 30, 31, 32, 33,  
45 34}. T-cell epitopes have been identified in both variable and constant domains {35, 36}.

Preferred MOMP proteins for use with the invention comprise an amino acid sequence: (a) having  
50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%,  
96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 25; and/or (b) which is a fragment of at least

*n* consecutive amino acids of SEQ ID NO: 25, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These MOMP proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 25. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 25, preferably one or more of the 5 B cell or T cell epitopes identified above. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 25. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain). Other preferred 10 fragments include one or more of the conserved constant regions identified above.

***SEQ ID NO: 25 (MOMP)(CT681)***

MKKLLKSVLVFAALSSASSLQALPVGNPAEPSLMIDGILWEGFGGDPCDPATWCDAISM RVGYYGDFVF  
DRVLKTDVNKEFQMGAKPTTDGNSAAPSTLTARENPAYGRHMQDAEMFTNAACMALNIWDRFDVFCTLG  
15 ATSGYLKGNSASFNLVGLPGDNENQKTVKAESVPNMSFDQSVVELYDTTFAWSVGARAALWECGCATLG  
ASFQYAQS PKVBEELNVLCNAAEFTINKPKGYVGKEFPLDLTAGTDAATGTKDASIDYHEWQASL ALSYR  
LNMFPTPYIGVKWSRASF DADTIRIAQPKSATAIFDTTTLNPTIAGAGDVKTGAEGQLGDTMQIVSLQLNK  
MKSRKSCGIAVGTTIVDADKYAVT VETRLIDERAAHVNAQFRF

**(4) *Cap1* (CT529)**

20 The *Chlamydia trachomatis* Cap1 protein corresponds with the hypothetical open reading frame CT 529 and refers to Class I Accessible Protein-1. See Ref. 37. One example of a Cap1 protein is set forth herein as SEQ ID NO: 26. Predicted T-cell epitopes of Cap1 are identified in this reference as CSFIGGITYL, preferably SFIGGITYL, and SIIGGITYL.

Preferred Cap1 proteins for use with the invention comprise an amino acid sequence: (a) having 50% 25 or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 26; and/or (b) which is a fragment of at least *n* consecutive amino acids of SEQ ID NO: 26, wherein *n* is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These Cap1 proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 26. Preferred fragments 30 of (b) comprise an epitope from SEQ ID NO: 26. Preferred T-cell epitopes include one or more of the T-cell epitopes identified above. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 26. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

***SEQ ID NO: 26 (Cap1)(CT529)***

MASICGRLGSGTGNALKAFFTQPNNKMARVVNKTGMDKTIKVAKSAAELTANILEQAGGAGSSAHITAS

QVSKGLGDARTVALGNAFNGALPGTVQSAQSFFSHMKAASQKTQEGDEGLTADLCVSHKRRAAAACSI  
IGGITYLATFGAIRPILFVNKMLAKPFLSSQTKANMGSSVSYIMAANHAASVVGAGLAIASAERADCEARC  
ARIAREESLLEVPGEEENACEKKVAGEKAKTFTRIKYALLTMLEKFLECADVFKLVLPLITMGIRAI  
GCTFTSAIIGLCTFCARA

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**(5) GroEL-like hsp60 protein**

One example of a *Chlamydia trachomatis* GroEL-like hsp60 protein is set forth herein as SEQ ID NO: 27. The role of Hsp60 in chlamydial infection is further described in, for example, 38, 39, 40, 41, and 42. Immunization of guinea pig models with recombinant Hsp60 is described in 43. B-cell epitopes of Hsp60 are identified in 44.

Preferred hsp60 proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 27; and/or (b) which is a fragment of at least  $n$  consecutive amino acids of SEQ ID NO: 27, wherein  $n$  is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 15, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These hsp60 proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 27. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 27, including one or more of the epitopes identified in the references discussed above. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 27. Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain). Other preferred fragments comprise a polypeptide sequence which does not cross-react with related human proteins.

**SEQ ID NO: 27 (groEL-like hsp60 protein)**

25 MVAKNIKYNEARKKIQKGVKTLAEAVKVTLGPGRHVVIDKSFGSPQVTKDGVTVAKEVBLADKHENMG  
AQMVKEVASKTADKAGDGTATVLAELAIVTEGLRNVTAGANPMDLKRGIDKAVKVVDQIRKISKPVQH  
HKEIAQVATISANNDAEIGNLIAEAMEKVGKNGSITVEEAKGFETVLDIVEGMNFNRGYLSSYPATNPET  
QECVLEDALVLIYDKKISGIKDFLPVLQQVAESGRPLLIIAEDIEGEALATLVNRIRGFRVCVKAPG  
30 FGDRRKAMEDIAILTGGQLISEELGMKLENANLAMLGKAKKVIWSKEDTTIVEGMGEKEALEARCESIK  
KQIEDSSSDYDKEKLQERLAKLSGGVAVIRGAATEIEMKEKKDRVDDAQHATIAAVEEGILPGGGTALI  
RCIPTLEAFLPMLTNEDEQIGARIVLKALSAPLKQIAANAGKEGAIIFQQVMSRSANEKYDALRDAYTDM  
LEAGILDPAKVTRSALESAAVAGLLLTTEALIAEIPEEKPAAPAMPAGMDY

**(6) 60 kDa Cysteine rich protein (OmcB) (CT443)**

35 One example of a *Chlamydia trachomatis* 60kDa Cysteine rich protein is set forth herein as SEQ ID NO: 28. This protein is also generally referred to as Omcb, Omp2 or CT 443. The role of Omcb in chlamydial infection is further described in, for example, 45, 46, 47, 48, and 49.

Preferred OmcB proteins for use with the invention comprise an amino acid sequence: (a) having 50% or more identity (e.g. 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5% or more) to SEQ ID NO: 28; and/or (b) which is a fragment of at least  $n$  consecutive amino acids of SEQ ID NO: 28, wherein  $n$  is 7 or more (e.g. 8, 10, 12, 14, 16, 18, 20, 5 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250 or more). These OmcB proteins include variants (e.g. allelic variants, homologs, orthologs, paralogs, mutants, etc.) of SEQ ID NO: 28. Preferred fragments of (b) comprise an epitope from SEQ ID NO: 28, including one or more of the epitopes identified in the references discussed above. Other preferred fragments lack one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the C-terminus and/or one or more amino acids (e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25 or more) from the N-terminus of SEQ ID NO: 28. 10 Other fragments omit one or more domains of the protein (e.g. omission of a signal peptide, of a cytoplasmic domain, of a transmembrane domain, or of an extracellular domain).

***SEQ ID NO: 28 (omp2/omcB)***

15 MRIGDPMNKLIRRATIFAVTSVASFASGVLETSMAESLSTNVISLADTKAKDNTSHKSKKARKNHSKE  
TPVDRKBFVAFVHESKATGPQDSCFGRMYTVKVNDRNVEITQAVPEYATVGSPYPIEITATGKRDCVDV  
IITQQLPCEAEFVRSDPATPTADGKLWVKIDRLGQGEKSKITVWVKPLKEGCCFTAATVCACPEIRSVT  
KCGQPAICVKQEGPENACLRCPVYKINIVNQGTATARVVVENVNPVPGYAHSSGQRVLFTLGDMQPGE  
HRTITVEPCPLKRGRTATNIATVSYCGGHKNTASVTTVINEPCVQVSIAGADWSYVCKPVYVISVSNPGD  
20 LVLRDVVVEDTLPGVTVLEAAGAQISCNKVVWTVKELNPGESLQYKVLVRAOTPQFTNNVVVKSCSDC  
GTCTSCABATTYWKGVAATHMCVVDTCDPVCVGENTVYRICVTNRGSAEDTNVSLMLKFSKELQPVSFSG  
PTKGTITGNTVVFDLSPRLGSKETVEFSVTLKAVSAGDARGEAILSSDTLTVPSDTENTHIY

There is an upper limit to the number of *Chlamydia trachomatis* antigens which will be in the compositions of the invention. Preferably, the number of *Chlamydia trachomatis* antigens in a composition of the invention is less than 20, less than 19, less than 18, less than 17, less than 16, less than 15, less than 14, less than 13, less than 12, less than 11, less than 10, less than 9, less than 8, less than 7, less than 6, less than 5, less than 4, or less than 3. Still more preferably, the number of *Chlamydia trachomatis* antigens in a composition of the invention is less than 6, less than 5, or less than 4.

30 The *Chlamydia trachomatis* antigens used in the invention are preferably isolated, i.e., separate and discrete, from the whole organism with which the molecule is found in nature or, when the polynucleotide or polypeptide is not found in nature, is sufficiently free of other biological macromolecules so that the polynucleotide or polypeptide can be used for its intended purpose.

***Fusion proteins***

35 The *Chlamydia trachomatis* antigens used in the invention may be present in the composition as individual separate polypeptides, but it is preferred that at least two (i.e. 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20) of the antigens are expressed as a single polypeptide chain (a

'hybrid' polypeptide). Hybrid polypeptides offer two principal advantages: first, a polypeptide that may be unstable or poorly expressed on its own can be assisted by adding a suitable hybrid partner that overcomes the problem; second, commercial manufacture is simplified as only one expression and purification need be employed in order to produce two polypeptides which are both antigenically useful.

The hybrid polypeptide may comprise two or more polypeptide sequences from the first antigen group. Accordingly, the invention includes a composition comprising a first amino acid sequence and a second amino acid sequence, wherein said first and second amino acid sequences are selected from a *Chlamydia trachomatis* antigen or a fragment thereof of the first antigen group. Preferably, the first and second amino acid sequences in the hybrid polypeptide comprise different epitopes.

The hybrid polypeptide may comprise two or more polypeptide sequences from the second antigen group. Accordingly, the invention includes a composition comprising a first amino acid sequence and a second amino acid sequence, wherein said first and second amino acid sequences are selected from a *Chlamydia trachomatis* antigen or a fragment thereof of the second antigen group. Preferably, the first and second amino acid sequences in the hybrid polypeptide comprise difference epitopes.

The hybrid polypeptide may comprise one or more polypeptide sequences from the first antigen group and one or more polypeptide sequences from the second antigen group. Accordingly, the invention includes a composition comprising a first amino acid sequence and a second amino acid sequence, said first amino acid sequence selected from a *Chlamydia trachomatis* antigen or a fragment thereof from the first antigen group and said second amino acid sequence selected from a *Chlamydia trachomatis* antigen or a fragment thereof from the second antigen group. Preferably, the first and second amino acid sequences in the hybrid polypeptide comprise difference epitopes.

The hybrid polypeptide may comprise one or more polypeptide sequences from the first antigen group and one or more polypeptide sequences from the third antigen group. Accordingly, the invention includes a composition comprising a first amino acid sequence and a second amino acid sequence, said first amino acid sequence selected from a *Chlamydia trachomatis* antigen or a fragment thereof from the first antigen group and said second amino acid sequence selected from a *Chlamydia trachomatis* antigen or a fragment thereof from the third antigen group. Preferably, the first and second amino acid sequences in the hybrid polypeptide comprise difference epitopes.

The hybrid polypeptide may comprise one or more polypeptide sequences from the second antigen group and one or more polypeptide sequences from the third antigen group. Accordingly, the invention includes a composition comprising a first amino acid sequence and a second amino acid sequence, said first amino acid sequence selected from a *Chlamydia trachomatis* antigen or a fragment thereof from the second antigen group and said second amino acid sequence selected from a

a *Chlamydia trachomatis* antigen or a fragment thereof from the third antigen group. Preferably, the first and second amino acid sequences in the hybrid polypeptide comprise difference epitopes.

Hybrids consisting of amino acid sequences from two, three, four, five, six, seven, eight, nine, or ten *Chlamydia trachomatis* antigens are preferred. In particular, hybrids consisting of amino acid 5 sequences from two, three, four, or five *Chlamydia trachomatis* antigens are preferred.

Different hybrid polypeptides may be mixed together in a single formulation. Within such combinations, a *Chlamydia trachomatis* antigen may be present in more than one hybrid polypeptide and/or as a non-hybrid polypeptide. It is preferred, however, that an antigen is present either as a hybrid or as a non-hybrid, but not as both.

10 Two-antigen hybrids for use in the invention may comprise: (1) PepA & LcrE; (2) PepA & OmpH-like; (3) PepA & L7/L12; (4) PepA & ArtJ; (5) PepA & DnaK; (6) PepA & CT398; (7) PepA & OmcA; (8) PepA & AtoS; (9) PepA & CT547; (10) PepA & Eno; (11) PepA & HrtA; (12) PepA & MurG; (13) LcrE & OmpH-like; (14) LcrE & L7/L12; (15) LcrE & ArtJ; (16) LcrE & DnaK; (17) LcrE & CT398; (18) LcrE & OmcA; (19) LcrE & AtoS; (20) LcrE & CT547; (21) LcrE & Eno; (22) LcrE & HrtA; (23) LcrE & MurG; (24) OmpH-like & L7/L12; (25) OmpH-like & ArtJ; (26) OmpH-like & DnaK; (27) OmpH-like & CT398; (28) OmpH-like & OmcA; (29) OmpH-like & AtoS; (30) OmpH-like & CT547; (31) OmpH-like & Eno; (32) OmpH-like & HrtA; (33) OmpH-like & MurG; (34) L7/L12 & ArtJ; (35) L7/L12 & DnaK; (36) L7/L12 & CT398; (37) L7/L12 & OmcA; (38) L7/L12 & AtoS; (39) L7/L12 & CT547; (40) L7/L12 & Eno; (41) L7/L12 & HrtA; (42) L7/L12 & MurG; (43) ArtJ & DnaK; (44) ArtJ & CT398; (45) ArtJ & OmcA; (46) ArtJ & AtoS; (47) ArtJ & CT547; (48) ArtJ & Eno; (49) ArtJ & HrtA; (50) ArtJ & MurG; (51) DnaK & CT398; (52) DnaK & OmcA; (53) DnaK & AtoS; (54) DnaK & CT547; (55) DnaK & Eno; (56) DnaK & HrtA; (57) DnaK & MurG; (58) CT398 & OmcA; (59) CT398 & AtoS; (60) CT398 & CT547; (61) CT398 & Eno; (62) CT398 & HrtA; (63) CT398 & MurG; (64) OmcA & AtoS; (65) OmcA & CT547; (66) OmcA & Eno; (67) OmcA & HrtA; (68) OmcA & MurG; (69) AtoS & CT547; (70) AtoS & Eno; (71) AtoS & HrtA; (72) AtoS & MurG; (73) CT547 & Eno; (74) CT547 & HrtA; (75) CT547 & MurG; (76) Eno & HrtA; (77) Eno & MurG; or (78) HrtA & MurG.

30 Hybrid polypeptides can be represented by the formula  $\text{NH}_2\text{-A}\text{-}\{\text{-X-L-}\}_n\text{-B-COOH}$ , wherein: X is an amino acid sequence of a *Chlamydia trachomatis* antigen or a fragment thereof from the first antigen group, the second antigen group or the third antigen group; L is an optional linker amino acid sequence; A is an optional N-terminal amino acid sequence; B is an optional C-terminal amino acid sequence; and n is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15.

If a -X- moiety has a leader peptide sequence in its wild-type form, this may be included or omitted in the hybrid protein. In some embodiments, the leader peptides will be deleted except for that of the

-X- moiety located at the N-terminus of the hybrid protein *i.e.* the leader peptide of X<sub>1</sub> will be retained, but the leader peptides of X<sub>2</sub> ... X<sub>n</sub> will be omitted. This is equivalent to deleting all leader peptides and using the leader peptide of X<sub>1</sub> as moiety -A-.

For each *n* instances of {-X-L-}, linker amino acid sequence -L- may be present or absent. For 5 instance, when *n*=2 the hybrid may be NH<sub>2</sub>-X<sub>1</sub>-L<sub>1</sub>-X<sub>2</sub>-L<sub>2</sub>-COOH, NH<sub>2</sub>-X<sub>1</sub>-X<sub>2</sub>-COOH, NH<sub>2</sub>-X<sub>1</sub>-L<sub>1</sub>-X<sub>2</sub>- COOH, NH<sub>2</sub>-X<sub>1</sub>-X<sub>2</sub>-L<sub>2</sub>-COOH, *etc.* Linker amino acid sequence(s) -L- will typically be short (*e.g.* 20 or fewer amino acids *i.e.* 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples comprise short peptide sequences which facilitate cloning, poly-glycine linkers (*i.e.* comprising Gly<sub>n</sub> where *n* = 2, 3, 4, 5, 6, 7, 8, 9, 10 or more), and histidine tags (*i.e.* His<sub>n</sub> where *n* = 3, 4, 5, 6, 7, 8, 9, 10 or more). Other suitable linker amino acid sequences will be apparent to those skilled in the art. A 10 useful linker is GSGGGG (SEQ ID 1), with the Gly-Ser dipeptide being formed from a *Bam*HI restriction site, thus aiding cloning and manipulation, and the (Gly)<sub>4</sub> tetrapeptide being a typical poly-glycine linker.

-A- is an optional N-terminal amino acid sequence. This will typically be short (*e.g.* 40 or fewer 15 amino acids *i.e.* 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples include leader sequences to direct protein trafficking, or short peptide sequences which facilitate cloning or purification (*e.g.* histidine tags *i.e.* His<sub>n</sub> where *n* = 3, 4, 5, 6, 7, 8, 9, 10 or more). Other suitable N-terminal amino acid 20 sequences will be apparent to those skilled in the art. If X<sub>1</sub> lacks its own N-terminus methionine, -A- is preferably an oligopeptide (*e.g.* with 1, 2, 3, 4, 5; 6, 7 or 8 amino acids) which provides a N-terminus methionine.

-B- is an optional C-terminal amino acid sequence. This will typically be short (*e.g.* 40 or fewer amino acids *i.e.* 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1). Examples include sequences to direct protein 25 trafficking, short peptide sequences which facilitate cloning or purification (*e.g.* comprising histidine tags *i.e.* His<sub>n</sub> where *n* = 3, 4, 5, 6, 7, 8, 9, 10 or more), or sequences which enhance protein stability. Other suitable C-terminal amino acid sequences will be apparent to those skilled in the art.

Most preferably, *n* is 2 or 3.

The invention also provides nucleic acid encoding hybrid polypeptides of the invention. Furthermore, 30 the invention provides nucleic acid which can hybridise to this nucleic acid, preferably under "high stringency" conditions (*e.g.* 65°C in a 0.1xSSC, 0.5% SDS solution).

Polypeptides of the invention can be prepared by various means (*e.g.* recombinant expression, purification from cell culture, chemical synthesis, *etc.*) and in various forms (*e.g.* native, fusions,

non-glycosylated, lipidated, etc.). They are preferably prepared in substantially pure form (i.e. substantially free from other chlamydial or host cell proteins).

Nucleic acid according to the invention can be prepared in many ways (e.g. by chemical synthesis, from genomic or cDNA libraries, from the organism itself, etc.) and can take various forms (e.g. 5 single stranded, double stranded, vectors, probes, etc.). They are preferably prepared in substantially pure form (i.e. substantially free from other chlamydial or host cell nucleic acids).

The term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones (e.g. phosphorothioates, etc.), and also peptide nucleic acids (PNA), etc. The invention includes nucleic acid comprising sequences complementary to those described above (e.g. 10 for antisense or probing purposes).

The invention also provides a process for producing a polypeptide of the invention, comprising the step of culturing a host cell transformed with nucleic acid of the invention under conditions which induce polypeptide expression.

The invention provides a process for producing a polypeptide of the invention, comprising the step of 15 synthesising at least part of the polypeptide by chemical means.

The invention provides a process for producing nucleic acid of the invention, comprising the step of amplifying nucleic acid using a primer-based amplification method (e.g. PCR).

The invention provides a process for producing nucleic acid of the invention, comprising the step of 20 synthesising at least part of the nucleic acid by chemical means.

20 **Strains**

Preferred polypeptides of the invention comprise an amino acid sequence found in *C.trachomatis* serovar D, or in one or more of an epidemiologically prevalent serotype.

Where hybrid polypeptides are used, the individual antigens within the hybrid (i.e. individual -X- 25 moieties) may be from one or more strains. Where n=2, for instance, X<sub>2</sub> may be from the same strain as X<sub>1</sub>, or from a different strain. Where n=3, the strains might be (i) X<sub>1</sub>=X<sub>2</sub>=X<sub>3</sub> (ii) X<sub>1</sub>=X<sub>2</sub>≠X<sub>3</sub> (iii) X<sub>1</sub>≠X<sub>2</sub>=X<sub>3</sub> (iv) X<sub>1</sub>≠X<sub>2</sub>≠X<sub>3</sub> or (v) X<sub>1</sub>=X<sub>3</sub>≠X<sub>2</sub>, etc.

**Heterologous host**

Whilst expression of the polypeptides of the invention may take place in *Chlamydia*, the invention 30 preferably utilises a heterologous host. The heterologous host may be prokaryotic (e.g. a bacterium) or eukaryotic. It is preferably *E.coli*, but other suitable hosts include *Bacillus subtilis*, *Vibrio cholerae*, *Salmonella typhi*, *Salmonella typhimurium*, *Neisseria lactamica*, *Neisseria cinerea*, *Mycobacteria* (e.g. *M.tuberculosis*), yeasts, etc.

*Immunogenic compositions and medicaments*

Compositions of the invention are preferably immunogenic compositions, and are more preferably vaccine compositions. The pH of the composition is preferably between 6 and 8, preferably about 7. The pH may be maintained by the use of a buffer. The composition may be sterile and/or 5 pyrogen-free. The composition may be isotonic with respect to humans.

Vaccines according to the invention may either be prophylactic (*i.e.* to prevent infection) or therapeutic (*i.e.* to treat infection), but will typically be prophylactic. Accordingly, the invention includes a method for the therapeutic or prophylactic treatment of *Chlamydia trachomatis* infection in an animal susceptible to chlamydial infection comprising administering to said animal a 10 therapeutic or prophylactic amount of the immunogenic compositions of the invention. Preferably, the immunogenic composition comprises a combination of *Chlamydia trachomatis* antigens, said combination selected from the group consisting of two, three, four, or all five *Chlamydia trachomatis* antigens of the first antigen group. Still more preferably, the combination consists of all five *Chlamydia trachomatis* antigens of the first antigen group.

15 Alternatively, the immunogenic composition comprises a combination of *Chlamydia trachomatis* antigens, said combination selected from the group consisting of two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, or thirteen *Chlamydia trachomatis* antigens selected from the second antigen group. Preferably, the combination is selected from the group consisting of three, four, or five *Chlamydia trachomatis* antigens selected from the second antigen group. Still more preferably, 20 the combination consists of five *Chlamydia trachomatis* antigens selected from the second antigen group.

Alternatively, the immunogenic composition comprises a combination of *Chlamydia trachomatis* antigens, said combination consisting of two, three, four, or five *Chlamydia trachomatis* antigens of the first antigen group and one, two, three, four, five or six *Chlamydia trachomatis* antigens of the 25 third antigen group. Preferably, the combination consists of three, four or five *Chlamydia trachomatis* antigens of the first antigen group and one, two, three, four, five or six *Chlamydia trachomatis* antigens of the third antigen group.

Alternatively, the immunogenic composition comprises a combination of *Chlamydia trachomatis* antigens, said combination consisting of two, three, four ,five, six, seven, eight, nine, ten, eleven, 30 twelve or thirteen *Chlamydia trachomatis* antigens of the second antigen group and one, two, three, four, five or six *Chlamydia trachomatis* antigens of the third antigen group. Preferably, the combination is selected from the group consisting of three, four, or five *Chlamydia trachomatis* antigens from the second antigen group and three, four or five *Chlamydia trachomatis* from the third antigen group. Still more preferably, the combination consists of five *Chlamydia trachomatis*

antigens from the second antigen group and three, four or five *Chlamydia trachomatis* antigens of the third antigen group.

The invention also provides a composition of the invention for use as a medicament. The medicament is preferably able to raise an immune response in a mammal (i.e. it is an immunogenic composition) and is more preferably a vaccine.

The invention also provides the use of the compositions of the invention in the manufacture of a medicament for raising an immune response in a mammal. The medicament is preferably a vaccine.

The invention also provides for a kit comprising a first component comprising a combination of *Chlamydia trachomatis* antigens. The combination of *Chlamydia trachomatis* antigens may be one or more of the immunogenic compositions of the invention. The kit may further include a second component comprising one or more of the following: instructions, syringe or other delivery device, adjuvant, or pharmaceutically acceptable formulating solution.

The invention also provides a delivery device pre-filled with the immunogenic compositions of the invention.

The invention also provides a method for raising an immune response in a mammal comprising the step of administering an effective amount of a composition of the invention. The immune response is preferably protective and preferably involves antibodies and/or cell-mediated immunity. The method may raise a booster response.

The mammal is preferably a human. Where the vaccine is for prophylactic use, the human is preferably a child (e.g. a toddler or infant) or a teenager; where the vaccine is for therapeutic use, the human is preferably a teenager or an adult. A vaccine intended for children may also be administered to adults e.g. to assess safety, dosage, immunogenicity, etc.

These uses and methods are preferably for the prevention and/or treatment of a disease caused by a *Chlamydia* (e.g. trachoma, pelvic inflammatory disease, epididymitis, infant pneumonia, etc.). The compositions may also be effective against *C.pneumoniae*.

One way of checking efficacy of therapeutic treatment involves monitoring *C.trachomatis* infection after administration of the composition of the invention. One way of checking efficacy of prophylactic treatment involves monitoring immune responses against the *Chlamydia trachomatis* antigens in the compositions of the invention after administration of the composition.

The vaccine compositions of the present invention can be evaluated in *in vitro* and *in vivo* animal models prior to host, e.g., human, administration. For example, *in vitro* neutralization by Peterson et al (1988) is suitable for testing vaccine compositions directed toward *Chlamydia trachomatis*.

One example of such an *in vitro* test is described as follows. Hyper-immune antisera is diluted in PBS containing 5% guinea pig serum, as a complement source. *Chlamydia trachomatis* ( $10^4$  IFU; inclusion forming units) are added to the antisera dilutions. The antigen-antibody mixtures are incubated at 37°C for 45 minutes and inoculated into duplicate confluent Hep-2 or HeLa cell monolayers contained in glass vials (e.g., 15 by 45 mm), which have been washed twice with PBS prior to inoculation. The monolayer cells are infected by centrifugation at 1000X g for 1 hour followed by stationary incubation at 37°C for 1 hour. Infected monolayers are incubated for 48 or 72 hours, fixed and stained with Chlamydia specific antibody, such as anti-MOMP. Inclusion-bearing cells are counted in ten fields at a magnification of 200X. Neutralization titer is assigned on the dilution that gives 50% inhibition as compared to control monolayers/IFU.

The efficacy of vaccine compositions can also be determined *in vivo* by challenging animal models of *Chlamydia trachomatis* infection, e.g., guinea pigs or mice, with the vaccine compositions. For example, *in vivo* vaccine composition challenge studies in the guinea pig model of *Chlamydia trachomatis* infection can be performed. A description of one example of this type of approach follows. Female guinea pigs weighing 450 – 500 g are housed in an environmentally controlled room with a 12 hour light-dark cycle and immunized with vaccine compositions via a variety of immunization routes. Post-vaccination, guinea pigs are infected in the genital tract with the agent of guinea pig inclusion conjunctivitis (GPIC), which has been grown in HeLa or McCoy cells (Rank et al. (1988)). Each animal receives approximately  $1.4 \times 10^7$  inclusion forming units (IFU) contained in 0.05 ml of sucrose-phosphate-glutamate buffer, pH 7.4 (Schacter, 1980). The course of infection monitored by determining the percentage of inclusion-bearing cells by indirect immunofluorescence with GPIC specific antisera, or by Giemsa-stained smear from a scraping from the genital tract (Rank et al 1988). Antibody titers in the serum is determined by an enzyme-linked immunosorbent assay.

Alternatively, *in vivo* vaccine compositions challenge studies can be performed in the murine model of *Chlamydia trachomatis* (Morrison et al 1995). A description of one example of this type of approach is as follows. Female mice 7 to 12 weeks of age receive 2.5 mg of depoprovera subcutaneously at 10 and 3 days before vaginal infection. Post-vaccination, mice are infected in the genital tract with 1,500 inclusion-forming units of *Chlamydia trachomatis* contained in 5ml of sucrose-phosphate-glutamate buffer, pH 7.4. The course of infection is monitored by determining the percentage of inclusion-bearing cells by indirect immunofluorescence with *Chlamydia trachomatis* specific antisera, or by a Giemsa-stained smear from a scraping from the genital tract of an infected mouse. The presence of antibody titers in the serum of a mouse is determined by an enzyme-linked immunosorbent assay.

Compositions of the invention will generally be administered directly to a patient. Direct delivery may be accomplished by parenteral injection (e.g. subcutaneously, intraperitoneally, intravenously, intramuscularly, or to the interstitial space of a tissue), or by rectal, oral (e.g. tablet, spray), vaginal,

topical, transdermal {e.g. see ref. 50} or transcutaneous {e.g. see refs. 51 & 52}, intranasal {e.g. see ref. 53}, ocular, aural, pulmonary or other mucosal administration.

The invention may be used to elicit systemic and/or mucosal immunity.

Dosage treatment can be a single dose schedule or a multiple dose schedule. Multiple doses may be  
5 used in a primary immunisation schedule and/or in a booster immunisation schedule. In a multiple dose schedule the various doses may be given by the same or different routes e.g. a parenteral prime and mucosal boost, a mucosal prime and parenteral boost, etc.

Chlamydial infections affect various areas of the body and so the compositions of the invention may be prepared in various forms. For example, the compositions may be prepared as injectables, either  
10 as liquid solutions or suspensions. Solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared (e.g. a lyophilised composition). The composition may be prepared for topical administration e.g. as an ointment, cream or powder. The composition may be prepared for oral administration e.g. as a tablet or capsule, as a spray, or as a syrup (optionally flavoured). The composition may be prepared for pulmonary administration e.g. as an  
15 inhaler, using a fine powder or a spray. The composition may be prepared as a suppository or pessary. The composition may be prepared for nasal, aural or ocular administration e.g. as drops. The composition may be in kit form, designed such that a combined composition is reconstituted just prior to administration to a patient. Such kits may comprise one or more antigens in liquid form and one or more lyophilised antigens.

20 Immunogenic compositions used as vaccines comprise an immunologically effective amount of antigen(s), as well as any other components, as needed. By 'immunologically effective amount', it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, age, the taxonomic group of individual to be treated  
25 (e.g. non-human primate, primate, etc.), the capacity of the individual's immune system to synthesise antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

*Further components of the composition*

30 The composition of the invention will typically, in addition to the components mentioned above, comprise one or more 'pharmaceutically acceptable carriers', which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolised macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers,  
35 and lipid aggregates (such as oil droplets or liposomes). Such carriers are well known to those of

ordinary skill in the art. The vaccines may also contain diluents, such as water, saline, glycerol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present. A thorough discussion of pharmaceutically acceptable excipients is available in reference 54.

5 Vaccines of the invention may be administered in conjunction with other immunoregulatory agents. In particular, compositions will usually include an adjuvant.

Preferred further adjuvants include, but are not limited to, one or more of the following set forth below:

A. Mineral Containing Compositions

10 Mineral containing compositions suitable for use as adjuvants in the invention include mineral salts, such as aluminium salts and calcium salts. The invention includes mineral salts such as hydroxides (e.g. oxyhydroxides), phosphates (e.g. hydroxyphosphates, orthophosphates), sulphates, etc. {e.g. see chapters 8 & 9 of ref. 55}), or mixtures of different mineral compounds, with the compounds taking any suitable form (e.g. gel, crystalline, amorphous, etc.), and with adsorption being preferred. The  
15 mineral containing compositions may also be formulated as a particle of metal salt. See ref. 56.

B. Oil-Emulsions

Oil-emulsion compositions suitable for use as adjuvants in the invention include squalene-water emulsions, such as MF59 (5% Squalene, 0.5% Tween 80, and 0.5% Span 85, formulated into submicron particles using a microfluidizer). See ref. 57.

20 Complete Freund's adjuvant (CFA) and incomplete Freund's adjuvant (IFA) may also be used as adjuvants in the invention.

C. Saponin Formulations

25 Saponin formulations, may also be used as adjuvants in the invention. Saponins are a heterologous group of sterol glycosides and triterpenoid glycosides that are found in the bark, leaves, stems, roots and even flowers of a wide range of plant species. Saponin from the bark of the *Quillaia saponaria* Molina tree have been widely studied as adjuvants. Saponin can also be commercially obtained from *Smilax ornata* (sarsaparilla), *Gypsophilla paniculata* (brides veil), and *Saponaria officinalis* (soap root). Saponin adjuvant formulations include purified formulations, such as QS21, as well as lipid formulations, such as ISCOMs.

30 Saponin compositions have been purified using High Performance Thin Layer Chromatography (HP-LC) and Reversed Phase High Performance Liquid Chromatography (RP-HPLC). Specific purified fractions using these techniques have been identified, including QS7, QS17, QS18, QS21, QH-A, QH-B and QH-C. Preferably, the saponin is QS21. A method of production of QS21 is disclosed in U.S. Patent No. 5,057,540. Saponin formulations may also comprise a sterol, such as cholesterol  
35 (see WO 96/33739).

Combinations of saponins and cholesterol can be used to form unique particles called Immunostimulating Complexes (ISCOMs). ISCOMs typically also include a phospholipid such as phosphatidylethanolamine or phosphatidylcholine. Any known saponin can be used in ISCOMs. Preferably, the ISCOM includes one or more of Quil A, QHA and QHC. ISCOMs are further described in EP 0 109 942, WO 96/11711 and WO 96/33739. Optionally, the ISCOMS may be devoid of additional detergent. See ref. 58.

5 A review of the development of saponin based adjuvants can be found at ref. 59.

C. Virosomes and Virus Like Particles (VLPs)

10 Virosomes and Virus Like Particles (VLPs) can also be used as adjuvants in the invention. These structures generally contain one or more proteins from a virus optionally combined or formulated with a phospholipid. They are generally non-pathogenic, non-replicating and generally do not contain any of the native viral genome. The viral proteins may be recombinantly produced or isolated from whole viruses. These viral proteins suitable for use in virosomes or VLPs include proteins derived from influenza virus (such as HA or NA), Hepatitis B virus (such as core or capsid proteins),  
15 Hepatitis E virus, measles virus, Sindbis virus, Rotavirus, Foot-and-Mouth Disease virus, Retrovirus, Norwalk virus, human Papilloma virus, HIV, RNA-phages, Q $\beta$ -phage (such as coat proteins), GA-phage, fr-phage, AP205 phage, and Ty (such as retrotransposon Ty protein p1). VLPs are discussed further in WO 03/024480, WO 03/024481, and Refs. 60, 61, 62 and 63. Virosomes are discussed further in, for example, Ref. 64

20 D. Bacterial or Microbial Derivatives

Adjuvants suitable for use in the invention include bacterial or microbial derivatives such as:

(1) *Non-toxic derivatives of enterobacterial lipopolysaccharide (LPS)*

Such derivatives include Monophosphoryl lipid A (MPL) and 3-O-deacylated MPL (3dMPL).  
25 3dMPL is a mixture of 3 De-O-acylated monophosphoryl lipid A with 4, 5 or 6 acylated chains. A preferred "small particle" form of 3 De-O-acylated monophosphoryl lipid A is disclosed in EP 0 689 454. Such "small particles" of 3dMPL are small enough to be sterile filtered through a 0.22 micron membrane (see EP 0 689 454). Other non-toxic LPS derivatives include monophosphoryl lipid A mimics, such as aminoalkyl glucosaminide phosphate derivatives e.g. RC-529. See Ref. 65.

(2) *Lipid A Derivatives*

30 Lipid A derivatives include derivatives of lipid A from *Escherichia coli* such as OM-174. OM-174 is described for example in Ref. 66 and 67.

(3) *Immunostimulatory oligonucleotides*

35 Immunostimulatory oligonucleotides suitable for use as adjuvants in the invention include nucleotide sequences containing a CpG motif (a sequence containing an unmethylated cytosine followed by guanosine and linked by a phosphate bond). Bacterial double stranded RNA or oligonucleotides containing palindromic or poly(dG) sequences have also been shown to be immunostimulatory.

The CpG's can include nucleotide modifications/analogs such as phosphorothioate modifications and can be double-stranded or single-stranded. Optionally, the guanosine may be replaced with an analog such as 2'-deoxy-7-deazaguanosine. See ref. 68, WO 02/26757 and WO 99/62923 for examples of possible analog substitutions. The adjuvant effect of CpG oligonucleotides is further discussed in Refs. 69, 70, WO 98/40100, U.S. Patent No. 6,207,646, U.S. Patent No. 6,239,116, and U.S. Patent No. 6,429,199.

The CpG sequence may be directed to TLR9, such as the motif GTCGTT or TTTCGTT. See ref. 71. The CpG sequence may be specific for inducing a Th1 immune response, such as a CpG-A ODN, or it may be more specific for inducing a B cell response, such a CpG-B ODN. CpG-A and CpG-B ODNs are discussed in refs. 72, 73 and WO 01/95935. Preferably, the CpG is a CpG-A ODN.

Preferably, the CpG oligonucleotide is constructed so that the 5' end is accessible for receptor recognition. Optionally, two CpG oligonucleotide sequences may be attached at their 3' ends to form "immunomers". See, for example, refs. 74, 75, 76 and WO 03/035836.

(4) *ADP-ribosylating toxins and detoxified derivatives thereof.*

Bacterial ADP-ribosylating toxins and detoxified derivatives thereof may be used as adjuvants in the invention. Preferably, the protein is derived from *E. coli* (i.e., *E. coli* heat labile enterotoxin "LT"), cholera ("CT"), or pertussis ("PT"). The use of detoxified ADP-ribosylating toxins as mucosal adjuvants is described in WO 95/17211 and as parenteral adjuvants in WO 98/42375. The toxin or toxoid is preferably in the form of a holotoxin, comprising both A and B subunits. Preferably, the A subunit contains a detoxifying mutation; preferably the B subunit is not mutated. Preferably, the adjuvant is a detoxified LT mutant such as LT-K63, LT-R72, and LTR192G. The use of ADP-ribosylating toxins and detoxified derivatives thereof, particularly LT-K63 and LT-R72, as adjuvants can be found in Refs. 77, 78, 79, 80, 81, 82, 83 and 84 each of which is specifically incorporated by reference herein in their entirety. Numerical reference for amino acid substitutions is preferably based on the alignments of the A and B subunits of ADP-ribosylating toxins set forth in Domenighini et al., Mol. Microbiol (1995) 15(6):1165 – 1167, specifically incorporated herein by reference in its entirety.

E. Human Immunomodulators

Human immunomodulators suitable for use as adjuvants in the invention include cytokines, such as interleukins (e.g. IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g. interferon- $\gamma$ ), macrophage colony stimulating factor, and tumor necrosis factor.

F. Bioadhesives and Mucoadhesives

Bioadhesives and mucoadhesives may also be used as adjuvants in the invention. Suitable bioadhesives include esterified hyaluronic acid microspheres (Ref. 85) or mucoadhesives such as cross-linked derivatives of poly(acrylic acid), polyvinyl alcohol, polyvinyl pyrrolidone, polysaccharides and carboxymethylcellulose. Chitosan and derivatives thereof may also be used as adjuvants in the invention. E.g., ref. 86.

G. Microparticles

Microparticles may also be used as adjuvants in the invention. Microparticles (*i.e.* a particle of ~100nm to ~150μm in diameter, more preferably ~200nm to ~30μm in diameter, and most preferably ~500nm to ~10μm in diameter) formed from materials that are biodegradable and non-toxic (*e.g.* a poly(α-hydroxy acid), a polyhydroxybutyric acid, a polyorthoester, a polyanhydride, a polycaprolactone, *etc.*), with poly(lactide-co-glycolide) are preferred, optionally treated to have a negatively-charged surface (*e.g.* with SDS) or a positively-charged surface (*e.g.* with a cationic detergent, such as CTAB).

H. Liposomes

10 Examples of liposome formulations suitable for use as adjuvants are described in U.S. Patent No. 6,090,406, U.S. Patent No. 5,916,588, and EP 0 626 169.

I. Polyoxyethylene ether and Polyoxyethylene Ester Formulations

15 Adjuvants suitable for use in the invention include polyoxyethylene ethers and polyoxyethylene esters. Ref. 87. Such formulations further include polyoxyethylene sorbitan ester surfactants in combination with an octoxynol (Ref. 88) as well as polyoxyethylene alkyl ethers or ester surfactants in combination with at least one additional non-ionic surfactant such as an octoxynol (Ref. 89).

Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether (laureth 9), polyoxyethylene-9-stearyl ether, polyoxyethylene-8-stearyl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether.

20 J. Polyphosphazene (PCPP)

PCPP formulations are described, for example, in Ref. 90 and 91.

K. Muramyl peptides

25 Examples of muramyl peptides suitable for use as adjuvants in the invention include N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), and N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine MTP-PE).

L. Imidazoquinolone Compounds.

Examples of imidazoquinolone compounds suitable for use adjuvants in the invention include Imiquamod and its homologues, described further in Ref. 92 and 93.

30 The invention may also comprise combinations of aspects of one or more of the adjuvants identified above. For example, the following adjuvant compositions may be used in the invention:

- (1) a saponin and an oil-in-water emulsion (ref. 94);
- (2) a saponin (*e.g.*, QS21) + a non-toxic LPS derivative (*e.g.*, 3dMPL) (see WO 94/00153);
- (3) a saponin (*e.g.*, QS21) + a non-toxic LPS derivative (*e.g.*, 3dMPL) + a cholesterol;

(4) a saponin (e.g. QS21) + 3dMPL + IL-12 (optionally + a sterol) (Ref. 95); combinations of 3dMPL with, for example, QS21 and/or oil-in-water emulsions (Ref. 96);

(5) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-block polymer L121, and thr-MDP, either microfluidized into a submicron emulsion or vortexed to generate a larger 5 particle size emulsion.

(6) Ribi<sup>TM</sup> adjuvant system (RAS), (Ribi Immunochem) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphoryl lipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox<sup>TM</sup>); and

10 (7) one or more mineral salts (such as an aluminum salt) + a non-toxic derivative of LPS (such as 3dPML).

Aluminium salts and MF59 are preferred adjuvants for parenteral immunisation. Mutant bacterial toxins are preferred mucosal adjuvants.

The composition may include an antibiotic.

15 **Further antigens**

The compositions of the invention may further comprise antigen derived from one or more sexually transmitted diseases in addition to *Chlamydia trachomatis*. Preferably the antigen is derived from one or more of the following sexually transmitted diseases: *N.gonorrhoeae* {e.g. 97, 98, 99, 100}; human papiloma virus; *Treponema pallidum*; herpes simplex virus (HSV-1 or HSV-2); HIV (HIV-1 or HIV-2); and *Haemophilus ducreyi*.

20 A preferred composition comprises: (1) at least *t* of the *Chlamydia trachomatis* antigens from either the first antigen group or the second antigen group, where *t* is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or 13, preferably *t* is five; (2) one or more antigens from another sexually transmitted disease. Preferably, the sexually transmitted disease is selected from the group consisting of herpes simplex virus; 25 preferably HSV-1 and/or HSV-2; human papillomavirus; *N.gonorrhoeae*; *Treponema pallidum*; and *Haemophilus ducreyi*. These compositions can thus provide protection against the following sexually-transmitted diseases: chlamydia, genital herpes, genital warts, gonorrhoea, syphilis and chancroid (See, Ref. 101).

Where a saccharide or carbohydrate antigen is used, it is preferably conjugated to a carrier protein in 30 order to enhance immunogenicity {e.g. refs. 102 to 111}. Preferred carrier proteins are bacterial toxins or toxoids, such as diphtheria or tetanus toxoids. The CRM<sub>197</sub> diphtheria toxoid is particularly preferred {112}. Other carrier polypeptides include the *N.meningitidis* outer membrane protein {113}, synthetic peptides {114, 115}, heat shock proteins {116, 117}, pertussis proteins {118, 119}, protein D from *H.influenzae* {120}, cytokines {121}, lymphokines, hormones, growth factors, toxin 35 A or B from *C.difficile* {122}, iron-uptake proteins {123}, etc. Where a mixture comprises capsular

saccharides from both serogroups A and C, it may be preferred that the ratio (w/w) of MenA saccharide:MenC saccharide is greater than 1 (e.g. 2:1, 3:1, 4:1, 5:1, 10:1 or higher). Different saccharides can be conjugated to the same or different type of carrier protein. Any suitable conjugation reaction can be used, with any suitable linker where necessary.

5 Toxic protein antigens may be detoxified where necessary e.g. detoxification of pertussis toxin by chemical and/or genetic means.

Where a diphtheria antigen is included in the composition it is preferred also to include tetanus antigen and pertussis antigens. Similarly, where a tetanus antigen is included it is preferred also to include diphtheria and pertussis antigens. Similarly, where a pertussis antigen is included it is preferred also to include diphtheria and tetanus antigens.

10 Antigens in the composition will typically be present at a concentration of at least 1 $\mu$ g/ml each. In general, the concentration of any given antigen will be sufficient to elicit an immune response against that antigen.

As an alternative to using protein antigens in the composition of the invention, nucleic acid encoding 15 the antigen may be used {e.g. refs. 124 to 132}. Protein components of the compositions of the invention may thus be replaced by nucleic acid (preferably DNA e.g. in the form of a plasmid) that encodes the protein.

***Definitions***

The term "comprising" means "including" as well as "consisting" e.g. a composition "comprising" X 20 may consist exclusively of X or may include something additional e.g. X + Y.

The term "about" in relation to a numerical value x means, for example,  $x \pm 10\%$ .

References to a percentage sequence identity between two amino acid sequences means that, when aligned, that percentage of amino acids are the same in comparing the two sequences. This alignment and the percent homology or sequence identity can be determined using software programs known in 25 the art, for example those described in section 7.7.18 of reference 133. A preferred alignment is determined by the Smith-Waterman homology search algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 2, BLOSUM matrix of 62. The Smith-Waterman homology search algorithm is disclosed in reference 134.

**EXAMPLE 1: Immunizations with Combinations of the First Antigen Group**

30 The five antigens of the first antigen group (OmpH-like protein, ArtJ, DnaK, CT398 and HrtA were prepared as described in reference 17. The antigens are expressed and purified. Compositions of antigen combinations are then prepared comprising five antigens per composition (and containing 15  $\mu$ g of each antigen per composition).

CD1 mice are divided into seven groups (5-6 mice per group for groups 1 through 4; 3 to 4 mice for groups 5, 6 and 7), and immunized as follows:

Group	Immunizing Composition	Route of Delivery
1	Mixture of 5 antigens (15 µg/each) + CFA	Intra-peritoneal
2	Mixture of 5 antigens (15 µg/each) + AlOH (200µg)	Intra-peritoneal
3	Mixture of 5 antigens (15 µg/each) + AlOH (200µg) + CpG (10µg)	Intra-peritoneal
4	Complete Freunds Adjuvant (CFA)	Intra-peritoneal
5	Mixture of 5 antigens (5 µg/each) + LTK63 (5µg)	Intranasal
6	AlOH (200µg) + CpG (10µg)	Intra-peritoneal
7	LTK63 (5µg)	Intranasal

5 Mice are immunized at two week intervals. Two weeks after the last immunization, all mice are challenged by intravaginal infection with *Chlamydia trachomatis* serovar D.

It will be understood that the invention has been described by way of example only and modifications may be made whilst remaining within the scope and spirit of the invention.

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